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## Title of Invention:

A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA LIBRARY. APPLICATION TO THE DETECTION OF MYCOBACTERIA

## Applicant(s) For DO/EO/US:

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Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. [X] This is a FIRST submission of items concerning a filing under 35 U.S.C. 371.
2. [ ] This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371.
3. [ ] This express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).
4. [X] A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. [X] A copy of the International Application as filed (35 U.S.C. 371(c)(2))
  - a. [X] is transmitted herewith (required only if not transmitted by the International Bureau).
  - b. [X] has been transmitted by the International Bureau.
  - c. [ ] is not required, as the application was filed in the United States Receiving Office (RO/US).
6. [ ] A translation of the International Application into English (35 U.S.C. 371(c)(2)).
7. [X] Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3)).
  - a. [ ] are transmitted herewith (required only if not transmitted by the International Bureau).
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  - c. [ ] have not been made; however, the time limit for making such amendments has NOT expired.
  - d. [X] have not been made and will not be made.
8. [ ] A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
9. [ ] An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).
10. [X] Annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).

## Items 11. to 16. below concern other document(s) or information included:

11. [ ] An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
12. [ ] An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
13. [ ] A FIRST preliminary amendment.  
[ ] A SECOND or SUBSEQUENT preliminary amendment.
14. [ ] A substitute specification.
15. [ ] A change of power of attorney and/or address letter.
16. [X] Other items or information:
  - a. [ ] Verified Small Entity Statement.
  - b. [ ] Copy of Notification of Missing Requirements.
  - c. [X] Copy of Cover Page of WIPO Publication (1 sheet).
  - d. [X] Sequence Listing (11 pages).

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17. [X] The following fees are submitted:

CALCULATIONS

**Basic National Fee (37 CFR 1.492(a)(1)-(5)):**

Search Report has been prepared by the EPO or JPO.....\$860.00  
 International preliminary examination fee paid to  
 USPTO (37 CFR 1.482).....\$690.00  
 No international preliminary examination fee paid to  
 USPTO (37 CFR 1.482) but international search fee  
 paid to USPTO (37 CFR 1.445(a)(2)).....\$760.00  
 Neither international preliminary examination fee  
 (37 CFR 1.482) nor international search fee  
 (37 CFR 1.445(a)(2)) paid to USPTO.....\$1,000.00  
 International preliminary examination fee paid to USPTO  
 (37 CFR 1.482) and all claims satisfied provisions  
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**ENTER APPROPRIATE BASIC FEE AMOUNT = \$ 860.00**

Surcharge of \$130.00 for furnishing the oath or declaration later than  
 [ ] 20 [ ] 30 months from the earliest claimed priority date  
 (37 CFR 1.492(e)).

Claims	Number Filed	Number Extra	Rate	
Total Claims	55 -20=	35	X \$18.00	\$ 630.00
Independent Claims	4 - 3=	1	X \$80.00	\$ 80.00
Multiple dependent claim(s) (if applicable)			+\$270.00	\$ 270.00
<b>TOTAL OF ABOVE CALCULATIONS</b>				<b>= \$1,840.00</b>

Reduction by 1/2 for filing by small entity, if applicable. Verified  
 Small Entity statement must also be filed. (Note 37 CFR 1.9, 1.27, 1.28)

**SUBTOTAL = \$1,840.00**

Processing fee of \$130.00 for furnishing the English translation later  
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**TOTAL NATIONAL FEE = \$1,840.00**

Fee for recording the enclosed assignment (37 CFR 1.21(h)). The  
 assignment must be accompanied by an appropriate cover sheet  
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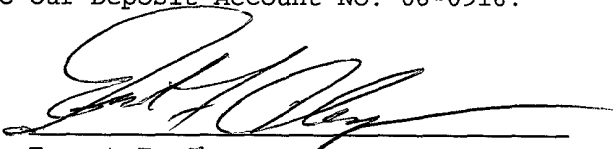
\$40.00 per property + \$  
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- a. [X] A check in the amount of **\$1,840.00** to cover the above fees is enclosed.  
 b. [ ] Please charge my Deposit Account No. \_\_\_\_\_ in the amount of  
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The Commissioner is hereby authorized to charge any other fees due under 37 C.F.R. §1.16  
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A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST  
FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-  
BASED DNA LIBRARY. APPLICATION TO THE DETECTION OF  
MYCOBACTERIA.

5

**I. Background of the invention**

The present invention pertains to a method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone belonging to a genomic DNA library of a given mycobacterium strain, said DNA library being cloned in a bacterial artificial chromosome (BAC). The invention concerns also polynucleotides identified by the above method, as well as detection methods for mycobacteria, particularly *Mycobacterium tuberculosis*, and kits using said polynucleotides as primers or probes. Finally, the invention deals with BAC-based mycobacterium DNA libraries used in the method according to the invention and particularly BAC-based *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG DNA libraries.

Radical measures are required to prevent the grim predictions of the World Health Organisation for the evolution of the global tuberculosis epidemic in the next century becoming a tragic reality. The powerful combination of genomics and bioinformatics is providing a wealth of information about the etiologic agent, *Mycobacterium tuberculosis*, that will facilitate the conception and development of new therapies. The start point for genome sequencing was the integrated map of the 4.4 Mb circular chromosome of the widely-used, virulent reference strain, *M. tuberculosis* H37Rv and appropriate cosmids were subjected to systematic shotgun sequence analysis at the Sanger Centre.

Cosmid clones (Balasubramanian et al., 1996; Pavelka et al., 1996) have played a crucial role in the *M. tuberculosis* H37Rv genome sequencing project. However, problems such as under-representation of certain regions of the chromosome, unstable inserts and the relatively small insert size complicated the production of a comprehensive set of canonical cosmids representing the entire genome.

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## II. Summary of the invention

In order to avoid the numerous technical constraints encountered in the state of the art, as described hereabove, when using genomic mycobacterial DNA libraries constructed in cosmid clones, the inventors have attempted to realize genomic mycobacterial DNA libraries in an alternative type of vectors, namely Bacterial Artificial Chromosome (BAC) vectors.

The success of this approach depended on whether the resulting BAC clones could maintain large mycobacterial DNA inserts. There are various reports describing the successful construction of a BAC library for eucaryotic organisms (Cai et al., 1995; Kim et al., 1996; Misumi et al., 1997; Woo et al., 1994; Zimmer et al., 1997) where inserts up to 725 kb (Zimmer et al., 1997) were cloned and stably maintained in the *E. coli* host strain.

Here, it is shown that, surprisingly, the BAC system can also be used for mycobacterial DNA, as 70% of the clones contained inserts in the size of 25 to 104 kb.

This is the first time that bacterial, and specifically mycobacterial, DNA is cloned in such BAC vectors.

In an attempt to obtain complete coverage of the genome with a minimal overlapping set of clones, a Bacterial Artificial Chromosome (BAC) library of *M. tuberculosis* was constructed, using the vector pBeloBAC11 (Kim et al., 1996) which combines a simple phenotypic screen for recombinant clones with the stable propagation of large inserts (Shizuya et al., 1992). The BAC cloning system is based on the *E. coli* F-factor, whose replication is strictly controlled and thus ensures stable maintenance of large constructs (Willets et al., 1987). BACs have been widely used for cloning of DNA from various eucaryotic species (Cai et al., 1995; Kim et al., 1996; Misumi et al., 1997; Woo et al., 1994; Zimmer et al., 1997). In contrast, to our knowledge this report describes the first attempt to use the BAC system for cloning bacterial DNA.

A central advantage of the BAC cloning system over cosmid vectors used in prior art is that the F-plasmid is present in only one or a maximum of two copies per cell, reducing the potential for recombination between DNA fragments and, more importantly, avoiding the lethal overexpression of cloned bacterial genes. However, the presence of the BAC as just a single copy means that plasmid DNA has to be extracted from a large volume of culture to obtain

sufficient DNA for sequencing and it is described here in the examples a simplified protocol to achieve this.

Further, the stability and fidelity of maintenance of the clones in the BAC library represent ideal characteristics for the identification of genomic differences possibly responsible for phenotypic variations in different mycobacterial species.

As it will be shown herein, BACs can be allied with conventional hybridization techniques for refined analyses of genomes and transcriptional activity from different mycobacterial species.

Having established a reliable procedure to screen for genomic polymorphisms, it is now possible to conduct these comparisons on a more systematic basis than in prior art using representative BACs throughout the chromosome and genomic DNA from a variety of mycobacterial species.

As another approach to display genomic polymorphisms, the inventors have also started to use selected H37Rv BACs for "molecular combing" experiments in combination with fluorescent *in situ* hybridization (Bensimon et al., 1994; Michalet et al., 1997). With such techniques the one skilled in the art is enabled to explore the genome of mycobacteria in general and of *M. tuberculosis* in particular for further polymorphic regions.

The availability of BAC-based genomic mycobacterial DNA libraries constructed by the inventors have allowed them to design methods and means both useful to identify genomic regions of interest of pathogenic mycobacteria, such as *Mycobacterium tuberculosis*, that have no counterpart in the corresponding non-pathogenic strains, such as *Mycobacterium bovis* BCG, and useful to detect the presence of polynucleotides belonging to a specific mycobacterium strain in a biological sample.

By a biological sample according to the present invention, it is notably intended a biological fluid, such as plasma, blood, urine or saliva, or a tissue, such as a biopsy.

Thus, a first object of the invention consists of a method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone belonging to a genomic DNA library of a given mycobacterium strain, said DNA library being cloned in a bacterial artificial chromosome (BAC).

The invention is also directed to a polynucleotide of interest that has been isolated according to the above method and in particular a polynucleotide containing one or several Open Reading Frames (ORFs), for example ORFs encoding either a polypeptide involved in the pathogenicity of a mycobacterium strain or ORFs encoding Polymorphic Glycine Rich Sequences (PGRS).

Such polynucleotides of interest may serve as probes or primers in order to detect the presence of a specific mycobacterium strain in a biological sample or to detect the expression of specific genes in a particular mycobacterial strain of interest.

The BAC-based genomic mycobacterial DNA libraries generated by the present inventors are also part of the invention, as well as each of the recombinant BAC clones and the DNA insert contained in each of said recombinant BAC clones.

The invention also pertains to methods and kits for detecting a specific mycobacterium in a biological sample using either at least one recombinant BAC clone or at least one polynucleotide according to the invention, as well as to methods and kits to detect the expression of one or several specific genes of a given mycobacterial strain present in a biological sample.

### III. Brief description of the Figures.

In order to better understand the present invention, reference will be made to the appended figures which depicted specific embodiments to which the present invention is in no case limited in scope with.

**Figures 1A and 1B :** PCR-screening for unique BAC clones with specific primers for 2 selected genomic regions of the H37Rv chromosome, using 21 pools representing 2016 BACs (Figure 1A) and sets of 20 subpools from selected positive pools (Figure 1B).

**Figure 2 :** Pulsed-field gel electrophoresis gel of *DraI*-cleaved BAC clones used for estimating the insert sizes of BACs.

**Figure 3 :** Minimal overlapping BAC map of *M. tuberculosis* H37Rv superimposed on the integrated physical and genetic map established by Philipp et al. (18). Y- and I- numbers show pYUB328 (2) and pYUB412 (16) cosmids which were shotgun sequenced during the H37Rv genome sequencing project. Y-cosmids marked with \* were shown in the integrated physical and genetic map



#### IV. Detailed description of the preferred embodiments.

As already mentioned hereinbefore, the present invention is directed to a method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and  
5 that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone belonging to a genomic DNA library of a given mycobacterium strain, said DNA library being cloned in a bacterial artificial chromosome (BAC) type vector.

10 For this purpose, the inventors have constructed several BAC-based mycobacterial genomic DNA libraries that may be used in order to perform the above described method.

Because it is the first time that mycobacterial genomic DNA has been successfully cloned in BAC type vectors, and because these DNA libraries are  
15 then novel and nonobvious, an object of the present invention consists in a mycobacterial genomic DNA library cloned in such a BAC type vector.

As an illustrative example, a BAC-based DNA library of *Mycobacterium tuberculosis* has been realized. Forty-seven cosmids chosen from the integrated map of the 4.4 Mb circular chromosome (Philipp et al., 1996a) were shotgun-  
20 sequenced during the initial phase of the H37Rv genome sequence project. The sequences of these clones were used as landmarks in the construction of a minimally overlapping BAC map. Comparison of the sequence data from the termini of 420 BAC clones allowed us to establish a minimal overlapping BAC map and to fill in the existing gaps between the sequence of cosmids. As well as  
25 using the BAC library for genomic mapping and sequencing, we also tested the system in comparative genomic experiments in order to uncover differences between two closely related mycobacterial species. As shown in a previous study (Philipp et al., 1996b), *M. tuberculosis*, *M. bovis* and *M. bovis* BCG, specifically BCG Pasteur strain, exhibit a high level of global genomic conservation, but  
30 certain polymorphic regions were also detected. Therefore, it was of great interest to find a reliable, easy and rapid way to exactly localize polymorphic regions in mycobacterial genomes using selected BAC clones. This approach was validated by determining the exact size and location of the polymorphisms in the genomic region of *DraI* fragment Z4 (Philipp et al., 1996b), taking advantage of the  
35 availability of an appropriate BAC clone covering the polymorphic region and

the H37Rv genome sequence data. This region is located approximately 1.7 Mb from the origin of replication.

The Bacterial Artificial Chromosome (BAC) cloning system is capable of stably propagating large, complex DNA inserts in *Escherichia coli*. As part of the *Mycobacterium tuberculosis* H37Rv genome sequencing project, a BAC library was constructed in the pBeloBAC11 vector and used for genome mapping, confirmation of sequence assembly, and sequencing. The library contains about 5000 BAC clones, with inserts ranging in size from 25 to 104 kb, representing theoretically a 70 fold coverage of the *M. tuberculosis* genome (4.4 Mb). A total of 840 sequences from the T7 and SP6 termini of 420 BACs were determined and compared to those of a partial genomic database. These sequences showed excellent correlation between the estimated sizes and positions of the BAC clones and the sizes and positions of previously sequenced cosmids and the resulting contigs. Many BAC clones represent linking clones between sequenced cosmids, allowing full coverage of the H37Rv chromosome, and they are now being shotgun-sequenced in the framework of the H37Rv sequencing project. Also, no chimeric, deleted or rearranged BAC clones were detected, which was of major importance for the correct mapping and assembly of the H37Rv sequence. The minimal overlapping set contains 68 unique BAC clones and spans the whole H37Rv chromosome with the exception of a single gap of ~ 150 kb. As a post-genomic application, the canonical BAC set was used in a comparative study to reveal chromosomal polymorphisms between *M. tuberculosis*, *M. bovis* and *M. bovis* BCG Pasteur, and a novel 12.7 kb segment present in *M. tuberculosis* but absent from *M. bovis* and *M. bovis* BCG was characterized. This region contains a set of genes whose products show low similarity to proteins involved in polysaccharide biosynthesis. The H37Rv BAC library therefore provides the one skilled in the art with a powerful tool both for the generation and confirmation of sequence data as well as for comparative genomics and a plurality of post-genomic applications.

The above described BAC-based *Mycobacterium tuberculosis* genomic DNA library is part of the present invention and has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on November 19, 1997 under the accession number I-1945.

Another BAC-based DNA library has been constructed with the genomic DNA of *Mycobacterium bovis* BCG, Pasteur strain, and said DNA library has

been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on June 30, 1998 under the accession number I-2049.

Thus, as a specific embodiment of the above described method for isolating a polynucleotide of interest said method makes use of at least one BAC-based DNA library that has been constructed from the genomic DNA of *Mycobacterium tuberculosis*, more specifically of the H37Rv strain and particularly of the DNA library deposited in the accession number I-1945.

In another specific embodiment of the above described method for isolating a polynucleotide of interest said method makes use of at least one BAC-based DNA library has been constructed from the genomic DNA of *Mycobacterium bovis* BCG, more specifically of the Pasteur strain and particularly of the DNA library deposited in the accession number I-2049.

In more details, the method according to the invention for isolating a polynucleotide of interest may comprise the following steps :

- a) isolating at least one polynucleotide contained in a clone of a BAC-based DNA library of mycobacterial origin;
- b) isolating :
  - at least one genomic or cDNA polynucleotide from a mycobacterium, said mycobacterium belonging to a strain different from the strain used to construct the BAC-based DNA library of step a); or alternatively
  - at least one polynucleotide contained in a clone of a BAC-based DNA library prepared from the genome of a mycobacterium that is different from the mycobacterium used to construct the BAC-based DNA library of step a);
- c) hybridizing the at least one polynucleotide of step a) to the at least one polynucleotide of step b);
- d) selecting the at least one polynucleotide of step a) that has not formed a hybrid complex with the at least one polynucleotide of step b);
- e) characterizing the selected polynucleotide.

Following the above procedure, the at least one polynucleotide of step a) may be prepared as follows :

- 1) digesting at least one recombinant BAC clone by an appropriate restriction endonuclease in order to isolate the polynucleotide insert of interest from the vector genetic material;
- 2) optionally amplifying the resulting polynucleotide insert;

3) optionally digesting the polynucleotide insert of step 1) or step 2) with at least one restriction endonuclease.

The above method of the invention allows the one skilled in the art to perform comparative genomics between different strains or species of mycobacteria cells, for example between pathogenic strains or species and their non pathogenic strains or species counterparts, as it is the illustrative case for the genomic comparison between *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG that is described herein in the examples.

Restriction digests of a given clone of a BAC library according to the invention may be blotted to membranes, and then probed with radiolabeled DNA from another strain or another species of mycobacteria, allowing the one skilled in the art to identify, characterize and isolate a polynucleotide of interest that may be involved in important metabolic and/or physiological pathways of the mycobacterium under testing, such as a polynucleotide functionally involved in the pathogenicity of said given mycobacteria for its host organism.

More specifically, the inventors have shown in Example 6 that when restriction digests of a given clone of the BAC library identified by the CNCM accession number I-1945 are blotted to membranes and then probed with radiolabeled total genomic DNA from, for example, *Mycobacterium bovis* BCG Pasteur, it is observed that restriction fragments that fail to hybridize with the *M. bovis* BCG Pasteur DNA are absent from its genome, hence identifying polymorphic regions between *M. bovis* BCG Pasteur and *M. tuberculosis* H37Rv.

Thus, a further object of the present invention consists in a polynucleotide of interest that has been isolated according to the method described herein before.

In Example 6, a polynucleotide of approximately 12.7 kilobases has been isolated that is present in the genome of *M. tuberculosis* but is absent of the genome of *M. bovis* BCG. This polynucleotide of interest contains 11 ORFs that may be involved in polysaccharide biosynthesis. In particular, two of said ORFs are of particular interest, namely ORF6 (MTCY277.33; Rv1511) that encodes a protein that shares significant homology with bacterial GDP-D-mannose dehydratases, whereas the protein encoded by ORF7 (MTCY277.34; Rv1512) shares significant homology with a nucleotide sugar epimerase. As polysaccharide is a major constituent of the mycobacterial cell wall, these deleted genes may cause the cell wall of *M. bovis* BCG to differ from that of *M. tuberculosis*, a fact that may have important consequences for both the immune

response to *M. bovis* BCG and virulence. Detection of such a polysaccharide is of diagnostic interest and possibly useful in the design of tuberculosis vaccines.

Consequently, the polynucleotide of interest obtained following the method according to the invention may contain at least one ORF, said ORF preferably encoding all or part of a polypeptide involved in an important  
5 metabolic and/or physiological pathway of the mycobacteria under testing, and more specifically all or part of a polypeptide that is involved in the pathogenicity of the mycobacteria under testing, such as for example *Mycobacterium tuberculosis*, and more generally mycobacteria belonging to the *Mycobacterium tuberculosis* complex.  
10

The *Mycobacterium tuberculosis* complex has its usual meaning, i.e. the complex of mycobacteria causing tuberculosis which are *Mycobacterium tuberculosis*, *Mycobacterium bovis*, *Mycobacterium africanum*, *Mycobacterium microti* and the vaccine strain *Mycobacterium bovis* BCG.

An illustrative polynucleotide of interest according to the present invention comprises all or part of the polynucleotide of approximately 12.7 kilobases that is present in the genome of *M. tuberculosis* but is absent from the genome of *M. bovis* BCG disclosed hereinbefore. This polynucleotide is contained in clone Rv58 of the BAC DNA library I-1945.  
15

Generally, the invention also pertains to a purified polynucleotide comprising the DNA insert contained in a recombinant BAC vector belonging to a BAC-based mycobacterial genomic DNA library, such as for example the I-1945 BAC DNA library.  
20

Advantageously, such a polynucleotide has been identified according to the method of the invention.  
25

Such a polynucleotide of interest may be used as a probe or a primer useful for specifically detecting a given mycobacterium of interest, such as *Mycobacterium tuberculosis* or *Mycobacterium bovis* BCG.

More specifically, the invention then deals with a purified polynucleotide useful as probe or a primer comprising all or part of the nucleotide sequence SEQ ID N°1.  
30

The location, on the *Mycobacterium tuberculosis* chromosome, of the above polynucleotide of sequence SEQ ID N°1 has now been ascribed to begin, at its 5'end at nucleotide at position nt 1696015 and to end, at its 3'end, at  
35 nucleotide at position nt 1708746.

For diagnostic purposes, this 12.7 kb deletion should allow a rapid PCR screening of tubercle isolates to identify whether they are bovine or human strains. The primers listed in Table 1 are flanking the deleted region and give a 722 bp amplicon in *M. bovis* or *M. bovis* BCG strains, but a fragment of 13,453 bp in *M. tuberculosis* that is practically impossible to amplify under the same PCR conditions. More importantly, assuming that some of the gene products from this region represent proteins with antigenic properties, it could be possible to develop a test that can reliably distinguish between the immune response induced by vaccination with *M. bovis* BCG vaccine strains and infection with *M. tuberculosis* or that the products (e.g. polysaccharides) are specific immunogens.

The invention also provides for a purified polynucleotide useful as a probe or as a primer, said polynucleotide being chosen in the following group of polynucleotides :

- a) a polynucleotide comprising at least 8 consecutive nucleotides of the sequence SEQ ID N°1;
- b) a polynucleotide whose sequence is fully complementary to the sequence of the polynucleotide defined in a);
- c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

For the purpose of defining a polynucleotide or oligonucleotide hybridizing under stringent hybridization conditions, such as above, it is intended a polynucleotide that hybridizes with a reference polynucleotide under the following hybridization conditions.

The hybridization step is realized at 65°C in the presence of 6 x SSC buffer, 5 x Denhardt's solution, 0,5% SDS and 100µg/ml of salmon sperm DNA.

For technical information, 1 x SSC corresponds to 0.15 M NaCl and 0.05M sodium citrate; 1 x Denhardt's solution corresponds to 0.02% Ficoll, 0.02% polyvinylpyrrolidone and 0.02% bovine serum albumin.

The hybridization step is followed by four washing steps :

- two washings during 5 min, preferably at 65°C in a 2 x SSC and 0.1%SDS buffer,
- one washing during 30 min, preferably at 65°C in a 2 x SSC and 0.1% SDS buffer,
- one washing during 10 min, preferably at 65°C in a 0.1 x SSC and 0.1%SDS buffer.

A first illustrative useful polynucleotide that is included in the polynucleotide of sequence SEQ ID N°1 is the polynucleotide of sequence SEQ ID N°2 that corresponds to the Sp6 end-sequence of SEQ ID N°1.

5 A second illustrative useful polynucleotide that is included in the polynucleotide of sequence SEQ ID N°1 is the polynucleotide of sequence SEQ ID N°3 that corresponds to the T7 end-sequence of SEQ ID N°1, located on the opposite strand.

10 The polynucleotide of sequence SEQ ID N°1 contains 11 ORFs, the respective locations of which, taking into account the orientation of each ORF on the chromosome, on the sequence of the *Mycobacterium tuberculosis* chromosome, is given hereafter :

- The location of ORF1 is comprised between nucleotide at position nt 1695944 and nucleotide at position nt1696441.
- The location of ORF2 is comprised between nucleotide at position nt 1696728 and nucleotide at position nt1697420.
- 15 - The location of ORF3 is comprised between nucleotide at position nt 1698096 and nucleotide at position nt1699892. ORF3 probably encodes a protein having the characteristics of a membrane protein.
- The location of ORF4 is comprised between nucleotide at position nt 1700210 and nucleotide at position nt1701088.
- 20 - The location of ORF5 is comprised between nucleotide at position nt 1701293 and nucleotide at position nt1702588. ORF5 encodes a protein having the characteristics of a membrane protein.
- The location of ORF6 is comprised between nucleotide at position nt 1703072 and nucleotide at position nt1704091. ORF6 encodes a protein having the characteristics of a GDP-D-mannose dehydratase.
- 25 - The location of ORF7 is comprised between nucleotide at position nt 1704091 and nucleotide at position nt1705056. ORF7 encodes a protein having the characteristics of a nucleotide sugar epimerase involved in colanic acid biosynthesis.
- 30 - The location of ORF8 is comprised between nucleotide at position nt 1705056 and nucleotide at position nt1705784.
- The location of ORF9 is comprised between nucleotide at position nt 1705808 and nucleotide at position nt1706593. ORF9 encodes a protein having the characteristics of colanic acid biosynthesis glycosyl transferase.
- 35

- The location of ORF10 is comprised between nucleotide at position nt 1706631 and nucleotide at position nt1707524.
- The location of ORF11 is comprised between nucleotide at position nt 1707530 and nucleotide at position nt1708648. ORF11 encodes a protein similar to a spore coat polysaccharide biosynthesis.

5 A polynucleotide of interest obtained by the above-disclosed method according to the invention may also contain at least one ORF that encodes all or part of acidic, glycine-rich proteins, belonging to the PE and PPE families, whose genes are often clustered and based on multiple copies of the polymorphic repetitive sequences. The names PE and PPE derive from the fact that the motifs ProGlu (PE, positions 8, 9) and ProProGlu (PPE, positions 7 to 9) are found near the N-terminus in almost all cases. The PE protein family all have a highly conserved N-terminal domain of ~110 amino acid residues, that is predicted to have a globular structure, followed by a C-terminal segment which varies in size, sequence and repeat copy number. Phylogenetic analysis separated the PE family into several groups, the larger of which is the highly repetitive PGRS class containing 55 members whereas the other groups share very limited sequence similarity in their C-terminal domains. The predicted molecular weights of the PE proteins vary considerably as a few members only contain the ~110 amino acid N-terminal domain while the majority have C-terminal extensions ranging in size from 100 up to >1400 residues. A striking feature of the PGRS proteins is their exceptional glycine content (up to 50%) due to the presence of multiple tandem repetitions of GlyGlyAla or GlyGlyAsn motifs or variations thereof.

10 Like the PE family, the PPE protein family also has a conserved N-terminal domain that comprises ~180 amino acid residues followed by C-terminal segments that vary considerably in sequence and length. These proteins fall into at least three groups, one of which constitutes the MPTR class characterised by the presence of multiple, tandem copies of the motif AsnXGlyXGlyAsnXGly. The second subgroup contains a characteristic, well-conserved motif around position 350 (GlyXXSerValProXXTrp), whereas the other group contains proteins that are unrelated except for the presence of the common 180-residue PPE domain. C-terminal extensions may range in size from 00 up to 3500 residues.

15 One member of the PGRS sub-family, the WHO antigen 22T (Abou-Zeid et al., 1991), a 55kD protein capable of binding fibronectin, is produced during

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disease and elicits a variable antibody response suggesting either that individuals mount different immune responses or that this PGRS-protein may not be produced in this form by all strains of *M. tuberculosis*. In other words, at least some PE\_PGRS coding sequences encode for proteins that are involved in the recognition of *M. tuberculosis* by the immune system of the infected host. Therefore, differences in the PGRS sequences could represent the principal source of antigenic variation in the otherwise genetically and antigenically homogeneous bacterium.

By performing the method of the invention using the *M. tuberculosis* BAC based DNA library I-1945, the inventors have discovered the occurrence of sequence differences between a given PGRS encoding ORF (ORF reference on the genomic sequence of *M. tuberculosis* Rv0746) of *M. tuberculosis* and its counterpart sequence in the genome of *M. bovis* BCG.

More precisely, the inventors have determined that one ORF contained in BAC vector N° Rv418 of the *M. tuberculosis* BCG I-1945 DNA library carries both base additions and base deletions when compared with the corresponding ORF in the genome of *M. bovis* BCG that is contained in the BAC vector N° X0175 of the *M. bovis* BCG I-2049 DNA library. The variations observed in the base sequences correspond to variations in the C-terminal part of the amino acid sequence of the PGRS ORF translation product.

As shown in Figure 6, an amino acid stretch of 9 residues in length is present in this *M. tuberculosis* PGRS (ORF reference Rv0746) and is absent from the ORF counterpart of *M. bovis* BCG, namely the following amino acid sequence:

NH<sub>2</sub>-GGAGGAGGSSAGGGGAGGAGGAGGWLLGD-COOH.

Furthermore, Figure 6 shows also that an amino acid stretch of 45 residues in length is absent from this *M. tuberculosis* PGRS and is present in the ORF counterpart of *M. bovis* BCG, namely following amino acid sequence:

NH<sub>2</sub>-GAGGIGGIGGNANGGAGGNGGTGGQLWGSGGAGVEGGAAL  
SVGDT-COOH.

Similar observations were made with PPE ORF Rv0442, which showed a 5 codon deletion relative to a *M. bovis* amino acid sequence.

Given that the polymorphism associated with the PE-PGRS or PEE ORFS resulted in extensive antigenic variability or reduced antigen presentation, this would be of immense significance for vaccine design, for understanding

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protective immunity in tuberculosis and, possibly, explain the varied responses seen in different BCG vaccination programmes.

There are several striking parallels between the PGRS proteins and the Epstein-Barr virus-encoded nuclear antigens (EBNA). Both polypeptide families are glycine-rich, contain Gly-Ala repeats that represent more than one third of the molecule, and display variation in the length of the repeat region between different isolates. The Gly-Ala repeat region of EBNA1 has been shown to function as a *cis*-acting inhibitor of antigen processing and MHC class I-restricted antigen presentation (Levitskaya et al., 1995). The fact that MHC class I knock-out mice are extremely susceptible to *M. tuberculosis* underlines the importance of MHC class I antigen presentation in protection against tuberculosis. Therefore, it is possible that the PE/PPE protein family also play some role in inhibiting antigen presentation, allowing the bacillus to hide from the host's immune system.

As such the novel and nonobvious PGRS polynucleotide from *M. bovis* which is homolog to the *M. tuberculosis* ORF Rv0746, and which is contained in the BAC clone N° X0175 (See Table 4 for SP6 and T7 end-sequences of clone n° X0175) of the I-2049 *M. bovis* BCG BAC DNA library is part of the present invention, as it represents a starting material in order to define specific probes or primers useful for detection of antigenic variability in mycobacterial strains, possible inhibition of antigen processing as well as to differentiate *M. tuberculosis* from *M. bovis* BCG.

Thus, a further object of the invention consists in a polynucleotide comprising the sequence SEQ ID N°4.

Polynucleotides of interest have been defined by the inventors as useful detection tools in order to differentiate *M. tuberculosis* from *M. bovis* BCG. Such polynucleotides are contained in the 45 aminoacid length coding sequence that is present in *M. bovis* BCG but absent from *M. tuberculosis*. This polynucleotide has a sequence beginning (5'end) at the nucleotide at position nt 729 of the sequence SEQ ID N°4 and ending (3'end) at the nucleotide in position nt 863 of the sequence SEQ ID N°4.

Thus, part of the present invention is also a polynucleotide which is chosen among the following group of polynucleotides :

a) a polynucleotide comprising at least 8 consecutive nucleotides of the nucleotide sequence SEQ ID N°5 ;

b) a polynucleotide which sequence is fully complementary to the sequence of the polynucleotide defined in a) ;

c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

5 The stringent hybridization conditions for the purpose of defining the above disclosed polynucleotide are defined herein before in the specification.

The invention also provides for a BAC-based *Mycobacterium tuberculosis* strain H37Rv genomic DNA library that has been deposited in the Collection Nationale de Cultures de Microorganismes on November 19, 1997 under the  
10 accession number I-1945.

A further object of the invention consists in a recombinant BAC vector which is chosen among the group consisting of the recombinant BAC vectors belonging to the BAC-based DNA library I-1945.

Generally, a recombinant BAC vector of interest may be chosen among  
15 the following set or group of BAC vectors contained in the BAC-based DNA library I-1945 :

Rv101; Rv102; Rv103; Rv104; Rv105; Rv106; Rv107; Rv108; Rv109; Rv10;  
Rv110; Rv111; Rv112; Rv113; Rv114; Rv115; Rv116; Rv117; Rv118; Rv119;  
Rv11; Rv120; Rv121; Rv122; Rv123; Rv124; Rv126; Rv127; Rv128; Rv129;  
20 Rv130; Rv132; Rv134; Rv135; Rv136; Rv137; Rv138; Rv139; Rv13; Rv140;  
Rv141; Rv142; Rv143; Rv144; Rv145; Rv146; Rv147; Rv148; Rv149; Rv14;  
Rv150; Rv151; Rv152; Rv153; Rv154; Rv155; Rv156; Rv157; Rv159; Rv15;  
Rv160; Rv161; Rv162; Rv163; Rv164; Rv165; Rv166; Rv167; Rv169; Rv16;  
Rv170; Rv171; Rv172; Rv173; Rv174; Rv175; Rv176; Rv177; Rv178; Rv179;  
25 Rv17; Rv180; Rv181; Rv182; Rv183; Rv184; Rv185; Rv186; Rv187; Rv188;  
Rv18; Rv190; Rv191; Rv192; Rv193; Rv194; Rv195; Rv196; Rv19; Rv1; Rv201;  
Rv204; Rv205; Rv207; Rv209; Rv20; Rv214; Rv215; Rv217; Rv218; Rv219;  
Rv21; Rv220; Rv221; Rv222; Rv223; Rv224; Rv225; Rv226; Rv227; Rv228;  
Rv229; Rv22; Rv230; Rv231; Rv232; Rv233; Rv234; Rv235; Rv237; Rv240;  
30 Rv241; Rv243; Rv244; Rv245; Rv246; Rv247; Rv249; Rv24; Rv251; Rv252;  
Rv253; Rv254; Rv255; Rv257; Rv258; Rv259; Rv25; Rv260; Rv261; Rv262;  
Rv263; Rv264; Rv265; Rv266; Rv267; Rv268; Rv269; Rv26; Rv270; Rv271;  
Rv272; Rv273; Rv274; Rv275; Rv276; Rv277; Rv278; Rv279; Rv27; Rv280;  
Rv281; Rv282; Rv283; Rv284; Rv285; Rv286; Rv287; Rv288; Rv289; Rv28;  
35 Rv290; Rv291; Rv292; Rv293; Rv294; Rv295; Rv296; Rv29; Rv2; Rv301;

Rv302; Rv303; Rv304; Rv306; Rv307; Rv308; Rv309; Rv30; Rv310; Rv311;  
 Rv312; Rv313; Rv314; Rv315; Rv316; Rv317; Rv318; Rv319; Rv31; Rv32;  
 Rv322; Rv327; Rv328; Rv329; Rv32; Rv330; Rv331; Rv333; Rv334; Rv335;  
 Rv336; Rv337; Rv338; Rv339; Rv33; Rv340; Rv341; Rv343; Rv344; Rv346;  
 5 Rv347; Rv348; Rv349; Rv34; Rv350; Rv351; Rv352; Rv353; Rv354; Rv355;  
 Rv356; Rv357; Rv358; Rv359; Rv35; Rv360; Rv361; Rv363; Rv364; Rv365;  
 Rv366; Rv367; Rv368; Rv369; Rv36; Rv370; Rv371; Rv373; Rv374; Rv375;  
 Rv376; Rv377; Rv378; Rv379; Rv37; Rv381; Rv382; Rv383; Rv384; Rv385;  
 Rv386; Rv387; Rv388; Rv389; Rv38; Rv390; Rv391; Rv392; Rv393; Rv396;  
 10 Rv39; Rv3; Rv40; Rv412; Rv413; Rv414; Rv415; Rv416; Rv417; Rv418; Rv419;  
 Rv41; Rv42; Rv43; Rv44; Rv45; Rv46; Rv47; Rv48; Rv49; Rv4; Rv50; Rv51;  
 Rv52; Rv53; Rv54; Rv55; Rv56; Rv57; Rv58; Rv59; Rv5; Rv60; Rv61; Rv62;  
 Rv63; Rv64; Rv65; Rv66; Rv67; Rv68; Rv69; Rv6; Rv70; Rv71; Rv72; Rv73;  
 Rv74; Rv75; Rv76; Rv77; Rv78; Rv79; Rv7; Rv80; Rv81; Rv82; Rv83; Rv84;  
 15 Rv85; Rv86; Rv87; Rv88; Rv89; Rv8; Rv90; Rv91; Rv92; Rv94; Rv95; Rv96;  
 Rv9.

The end sequences of the polynucleotide inserts of each of the above clones corresponding respectively to the sequences adjacent to the T7 promoter and to the Sp6 promoter on the BAC vector are shown in Table 3.

20 It has been shown by the inventors that the minimal overlapping set of BAC vectors of the BAC-based DNA library I-1945 contains 68 unique BAC clones and practically spans almost the whole H37Rv chromosome with the exception of a single gap of approximately 150 kb.

More specifically, a recombinant BAC vector of interest is chosen among  
 25 the following set or group of BAC vectors from the BAC-based DNA library I-1945, the location of which vector DNA inserts on the chromosome of *M. tuberculosis* is shown in Figure 3 :

Rv234; Rv351; Rv166; Rv35; Rv415; Rv404; Rv209; Rv272; Rv30; Rv228;  
 Rv233; Rv38; Rv280; Rv177; Rv48; Rv374; Rv151; Rv238; Rv156; Rv92; Rv3;  
 30 Rv403; Rv322; Rv243; Rv330; Rv285; Rv233; Rv219; Rv416; Rv67; Rv222;  
 Rv149; Rv279; Rv87; Rv273; Rv266; Rv25; Rv136; Rv414; Rv13; Rv289; Rv60;  
 Rv104; Rv5; Rv165; Rv215; Rv329; Rv240; Rv19; Rv74; Rv411; Rv167; Rv56;  
 Rv80; Rv164; Rv59; Rv313; Rv265; Rv308; Rv220; Rv258; Rv339; Rv121;  
 Rv419; Rv418; Rv45; Rv217; Rv134; Rv17; Rv103; Rv21; Rv22; Rv2; Rv270;  
 35 Rv267; Rv174; Rv257; Rv44; Rv71; Rv7; Rv27; Rv191; Rv230; Rv128; Rv407;

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Rv106; Rv39; Rv255; Rv74; Rv355; Rv268; Rv58; Rv173; Rv264; Rv417; Rv401; Rv144; Rv302; Rv81; Rv163; Rv281; Rv221; Rv420; Rv175; Rv86; Rv412; Rv73; Rv269; Rv214; Rv287; Rv42; Rv143.

The polynucleotides disclosed in Table 3 may be used as probes in order to select a given clone of the BAC DNA library I-1945 for further use.

The invention also provides for a BAC-based *Mycobacterium bovis* strain Pasteur genomic DNA library that has been deposited in the Collection Nationale de Cultures de Microorganismes on June 30, 1998 under the accession number I-2049.

A further object of the invention consists in a recombinant BAC vector which is chosen among the group consisting of the recombinant BAC vectors belonging to the BAC-based DNA library I-2049. This DNA library contains approximately 1600 clones. The average insert size is estimated to be ~80 kb.

Generally, a recombinant BAC vector of interest may be chosen among the following set or group of BAC vectors contained in the BAC-based DNA library I-2049 :

X0001; X0002; X0003; X0004; X0006; X0007; X0008; X0009; X0010; X0012; X0013; X0014; X0015; X0016; X0017; X0018; X0019; X0020; X0021; X0175.

The end sequences of the polynucleotide inserts of each of the above clones corresponding respectively to the sequences adjacent to the T7 promoter and to the Sp6 promoter on the BAC vector are shown in Table 4.

The polynucleotides disclosed in Table 4 may be used as probes in order to select a given clone of the BAC DNA library I-2049 for further use.

Are also part of the invention the polynucleotide inserts that are contained in the above described BAC vectors, that are useful as primers or probes.

These polynucleotides and nucleic acid fragments may be used as primers for use in amplification reactions, or as nucleic probes.

PCR is described in the US patent N° 4,683,202. The amplified fragments may be identified by an agarose or a polyacrylamide gel electrophoresis, or by a capillary electrophoresis or alternatively by a chromatography technique (gel filtration, hydrophobic chromatography or ion exchange chromatography). The specificity of the amplification may be ensured by a molecular hybridization using, for example, one of the initial primers as nucleic probes.

Amplified nucleotide fragments are used as probes in hybridization reactions in order to detect the presence of one polynucleotide according to the

present invention or in order to detect mutations in the genome of the given mycobacterium of interest, specifically a mycobacterium belonging to the *Mycobacterium tuberculosis* complex and more specifically *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG.

5 Are also part of the present invention the amplified nucleic fragments (« amplicons ») defined herein above.

These probes and amplicons may be radioactively or non-radioactively labeled, using for example enzymes or fluorescent compounds.

10 Other techniques related to nucleic acid amplification may also be used and are generally preferred to the PCR technique.

The Strand Displacement Amplification (SDA) technique (Walker et al., 1992) is an isothermal amplification technique based on the ability of a restriction enzyme to cleave one of the strands at his recognition site (which is under a hemiphosphorothioate form) and on the property of a DNA polymerase to initiate the synthesis of a new strand from the 3'OH end generated by the restriction enzyme and on the property of this DNA polymerase to displace the previously synthesized strand being localized downstream. The SDA method comprises two main steps :

- 15 a) The synthesis, in the presence of dCTP-alpha-S, of DNA molecules that are flanked by the restriction sites that may be cleaved by an appropriate enzyme.
- 20 b) The exponential amplification of these DNA molecules modified as such, by enzyme cleavage, strand displacement and copying of the displaced strands. The steps of cleavage, strand displacement and copy are repeated a sufficient number of times in order to obtain an accurate sensitivity of the assay.

25 The SDA technique was initially realized using the restriction endonuclease HincII but is now generally practised with an endonuclease from *Bacillus stearothermophilus* (BSOBI) and a fragment of a DNA polymerase which is devoid of any 5'→3'exonuclease activity isolated from *Bacillus cladothax* (exo- Bca) [=exo-minus-Bca]. Both enzymes are able to operate at

30 60°C and the system is now optimized in order to allow the use of dUTP and the decontamination by UDG. When using this technique, as described by Spargo et al. in 1996, the doubling time of the target DNA is of 26 seconds and the amplification rate is of  $10^{10}$  after an incubation time of 15 min at 60°C.

The SDA amplification technique is more easy to perform than PCR (a single thermostated waterbath device is necessary) and is faster than the other amplification methods.

Thus, another object of the present invention consists in using the nucleic acid fragments according to the invention (primers) in a method of DNA or RNA amplification according to the SDA technique. For performing SDA, two pairs of primers are used : a pair of external primers (B1, B2) consisting of a sequence specific for the target polynucleotide of interest and a pair of internal primers (S1, S2) consisting of a fusion oligonucleotide carrying a site that is recognized by a restriction endonuclease, for example the enzyme BSOBI.

The operating conditions to perform SDA with such primers are described in Spargo et al, 1996.

The polynucleotides of the invention and their above described fragments, especially the primers according to the invention, are useful as technical means for performing different target nucleic acid amplification methods such as :

- TAS (Transcription-based Amplification System), described by Kwoh et al. in 1989.
- SR (Self-Sustained Sequence Replication), described by Guatelli et al. in 1990.
- NASBA (Nucleic acid Sequence Based Amplification), described by Kievitis et al. in 1991.
- TMA (Transcription Mediated Amplification).

The polynucleotides according to the invention are also useful as technical means for performing methods for amplification or modification of a nucleic acid used as a probe , such as :

- LCR (Ligase Chain Reaction), described by Landegren et al. in 1988 and improved by Barany et al. in 1991 who employ a thermostable ligase.
- RCR (Repair Chain Reaction) described by Segev et al. in 1992.
- CPR (Cycling Probe Reaction), described by Duck et al. in 1990.
- Q-beta replicase reaction, described by Miele et al. in 1983 and improved by Chu et al. in 1986, Lizardi et al. in 1988 and by Burg et al. and Stone et al. in 1996.

When the target polynucleotide to be detected is a RNA, for example a mRNA, a reverse transcriptase enzyme will be used before the amplification reaction in order to obtain a cDNA from the RNA contained in the biological sample. The generated cDNA is subsequently used as the nucleic acid target for

the primers or the probes used in an amplification process or a detection process according to the present invention.

The non-labeled polynucleotides or oligonucleotides of the invention may be directly used as probes. Nevertheless, the polynucleotides or oligonucleotides are generally labeled with a radioactive element ( $^{32}\text{P}$ ,  $^{35}\text{S}$ ,  $^3\text{H}$ ,  $^{125}\text{I}$ ) or by a non-isotopic molecule (for example, biotin, acetylaminofluorene, digoxigenin, 5-bromodesoxyuridin, fluorescein) in order to generate probes that are useful for numerous applications.

Examples of non-radioactive labeling of nucleic acid fragments are described in the french patent N° FR-7810975 or by Urdea et al. or Sanchez-Pescador et al., 1988.

In the latter case, other labeling techniques may be also used such as those described in the french patents FR-2 422 956 and 2 518 755. The hybridization step may be performed in different ways (Matthews et al., 1988). The more general method consists of immobilizing the nucleic acid that has been extracted from the biological sample onto a substrate (nitrocellulose, nylon, polystyrene) and then to incubate, in defined conditions, the target nucleic acid with the probe. Subsequently to the hybridization step, the excess amount of the specific probe is discarded and the hybrid molecules formed are detected by an appropriate method (radioactivity, fluorescence or enzyme activity measurement).

Advantageously, the probes according to the present invention may have structural characteristics such that they allow the signal amplification, such structural characteristics being, for example, branched DNA probes as those described by Urdea et al. in 1991 or in the European patent N° EP-0 225 807 (Chiron).

In another advantageous embodiment of the probes according to the present invention, the latters may be used as « capture probes », and are for this purpose immobilized on a substrate in order to capture the target nucleic acid contained in a biological sample. The captured target nucleic acid is subsequently detected with a second probe which recognizes a sequence of the target nucleic acid which is different from the sequence recognized by the capture probe.

The oligonucleotide probes according to the present invention may also be used in a detection device comprising a matrix library of probes immobilized on a substrate, the sequence of each probe of a given length being localized in a shift of one or several bases, one from the other, each probe of the matrix library thus

being complementary to a distinct sequence of the target nucleic acid. Optionally, the substrate of the matrix may be a material able to act as an electron donor, the detection of the matrix positions in which an hybridization has occurred being subsequently determined by an electronic device. Such matrix libraries of probes  
5 and methods of specific detection of a target nucleic acid is described in the European patent application N° EP-0 713 016 (Affymax technologies) and also in the US patent N° US-5,202,231 (Drmanac).

Since almost the whole length of a mycobacterial chromosome is covered by a BAC-based genomic DNA libraries according to the present invention (i.e. 97% of  
10 the *M. tuberculosis* chromosome is covered by the BAC library I-1945), these DNA libraries will play an important role in a plurality of post-genomic applications, such as in mycobacterial gene expression studies where the canonical set of BACs could be used as a matrix for hybridization studies. Probing such matrices with cDNA probes prepared from total mRNA will uncover genetic loci induced or repressed  
15 under different physiological conditions (Chuang et al., 1993; Trieselmann et al., 1992). As such, the H37Rv BAC library represents a fundamental resource for present and future genomics investigations.

The BAC vectors or the polynucleotide inserts contained therein may be directly used as probes, for example when immobilized on a substrate such as  
20 described herein before.

The BAC vectors or their polynucleotide inserts may be directly adsorbed on a nitrocellulose membrane, at predetermined locations on which one or several polynucleotides to be tested are then put to hybridize therewith.

Preferably, a collection of BAC vectors that spans the whole genome of  
25 the mycobacterium under testing will be immobilized, such as, for example, the set of 68 BAC vectors of the I-1945 DNA library that is described elsewhere in the specification and shown in Figure 3.

The immobilization and hybridization steps may be performed as described in the present Materials and Methods Section.

30 As another illustrative embodiment of the use of the BAC vectors of the invention as polynucleotide probes, these vectors may be useful to perform a transcriptional activity analysis of mycobacteria growing in different environmental conditions, for example under conditions in which a stress response is expected, as it is the case at an elevated temperature, for example  
35 40°C.

In this specific embodiment of the invention, Genescreen membranes may be used to immobilize the restriction endonuclease digests (*Hind*III digests for the BAC DNA library I-1945) of the BAC vectors by transfer from a gel (Trieselmann et al., 1992).

5 Alternatively, the BAC vectors may be immobilized for dot blot experiments as follows. First, the DNA concentration of each BAC clone is determined by hybridization of blots of clone DNAs and of a BAC vector concentration standard with a BAC vector specific DNA probe. Hybridization is quantified by the Betascope 603 blot analyzer (Betagen Corp.), which collects  
10 beta particles directly from the blot with high efficiency. Then, 0.5 µg of each clone DNA is incubated in 0.25 M NaOH and 10 mM EDTA at 65°C for 60 min to denature the DNA and degrade residual RNA contaminants. By using a manifold filtration system (21 by 21 wells), each clone DNA is blotted onto a GeneScreen Plus nylon membrane in the alkaline solution. After neutralization,  
15 the blots are baked at 85°C for 2 h under vacuum. Positive and negative controls are added when necessary. In order to perform this procedure, it may be referred to the article of Chuang et al. (1993).

For RNA extractions, cells grown in a suitable volume of culture medium may, for example, be immediately mixed with an equal volume of crushed ice at -  
20 70°C and spun at 4°C in a 50 ml centrifugation tube. The cell pellet is then suspended in 0.6 ml of ice-cold buffer (10 mM KCl, 5 mM MgCl<sub>2</sub>, 10 mM Tris; pH 7.4) and then immediately added to 0.6 ml of hot lysis buffer (0.4 M NaCl, 40 mM EDTA, 1% beta-mercaptoethanol, 1% SDS, 20 mM Tris; pH 7.4) containing 100 µl of water saturated phenol. This mixture is incubated in a boiling water  
25 bath for 40 s. The debris are removed by centrifugation. The supernatant is extracted with phenol-chloroform five times, ethanol precipitated, and dried. The dried RNA pellet is dissolved in water before use.

Then labeled total cDNA may be prepared by the following method. The reaction mixture contains 15 µg of the previously prepared total RNA, 5 µg of  
30 pd(N<sub>6</sub>) (random hexamers from Pharmacia Inc.), 0.5 mM dATP, 0.5 mM dGTP and 0.5mM DTTP, 5µM dCTP, 100 µCi of [ $\alpha$ -<sup>32</sup>P]dCTP (3,000 Ci/mmol), 50 mM Tris-HCl (pH 8.3), 6 mM MgCl<sub>2</sub>, 40 mM KCl, 0.5 U of avian myeloblastosis virus reverse transcriptase (Life Science Inc.) in a total volume of 50 µl. The reaction is allowed to continue overnight at room temperature. EDTA and NaOH  
35 are then added to final concentrations of 50 mM and 0.25 M, respectively, and

the mixture is incubated at 65°C for 30 min to degrade the RNA templates. The cDNA is then ready to use after neutralization by adding Hcl and Tris buffer.

The hybridization step may be performed as described by Chuang et al. (1993) and briefly disclosed hereinafter. The DNA dot blot is hybridized to <sup>32</sup>P-labeled total cDNA in a solution containing 0.1% polyvinylpyrrolidone, 0.1% Ficoll, 0.1% sodium Pp<sub>i</sub>, 0.1% bovine serum albumin, 0.5% SDS, 100 mM NaCl, and 0.1 mM sodium citrate, pH 7.2, at 65°C for 2 days and then washed with a solution containing 0.1% SDS, 100 mM NaCl, and 10 mM Na-citrate, pH 7.2. The same dot blot is used for hybridization with both control and experimental cDNAs, with an alkaline probe stripping procedure (soaked twice in 0.25M NaOH-0.75 M NaCl at room temperature, 30 min each, neutralized, and completely dried at 65°C for at least 30 min) between the two hybridizations. Quantification may be done with the Betascope 603 blot analyzer (Betagen Corp.).

As it flows from the above technical teachings, another object of the invention consists in a method for detecting the presence of mycobacteria in a biological sample comprising the steps of :

- a) bringing into contact the recombinant BAC vector or a purified polynucleotide according to the invention with a biological sample ;
- b) detecting the hybrid nucleic acid molecule formed between said purified polynucleotide and the nucleic acid molecules contained within the biological sample.

The invention further deals with a method for detecting the presence of mycobacteria in a biological sample comprising the steps of :

- a) bringing into contact the recombinant BAC vector or a purified polynucleotide according to the invention that has been immobilized onto a substrate with a biological sample ;
- b) bringing into contact the hybrid nucleic acid molecule formed between said purified polynucleotide and the nucleic acid contained in the biological sample with a labeled recombinant BAC vector or a polynucleotide according to the invention, provided that said polynucleotide and polynucleotide of step a) have non-overlapping sequences.

Another object of the invention consists in a method for detecting the presence of mycobacteria in a biological sample comprising the steps of :

- a) bringing into contact the nucleic acid molecules contained in the biological sample with a pair of primers according to the invention;  
b) amplifying said nucleic acid molecules;  
c) detecting the nucleic acid fragments that have been amplified, for example by gel electrophoresis or with a labeled polynucleotide according to the invention.

In one specific embodiment of the above detection and/or amplification methods, said methods comprise an additional step wherein before step a), the nucleic acid molecules of the biological sample have been made available to a hybridization reaction.

- In another specific embodiment of the above detection methods, said methods comprise an additional step, wherein, before the detection step, the nucleic acid molecules that are not hybridized with the immobilized purified polynucleotide are removed.

Also part of the invention is a kit for detecting mycobacteria in a biological sample comprising :

- a) a recombinant BAC vector or a purified polynucleotide according to the invention;  
b) reagents necessary to perform a nucleic acid hybridization reaction.

The invention also pertains to a kit for detecting a mycobacteria in a biological sample comprising :

- a) a recombinant BAC vector or a purified polynucleotide according to the invention that is immobilized onto a substrate;  
b) reagents necessary to perform a nucleic acid hybridization reaction;  
c) a purified polynucleotide according to the invention which is radioactively or non-radioactively labeled, provided that said polynucleotide and the polynucleotide of step a) have non-overlapping sequences.

Moreover, the invention provides for a kit for detecting mycobacteria in a biological sample comprising :

- a) a pair of purified primers according to the invention;  
b) reagents necessary to perform a nucleic acid amplification reaction;  
c) optionally, a purified polynucleotide according to the invention useful as a probe.

The invention embraces also a method for detecting the presence of a genomic DNA, a cDNA or a mRNA of mycobacteria in a biological sample, comprising the steps of :

- a) bringing into contact the biological sample with a plurality of BAC vectors according to the invention or purified polynucleotides according to the invention, that are immobilized on a substrate;
- b) detecting the hybrid complexes formed.

5       The invention also provides a kit for detecting the presence of genomic DNA, cDNA or mRNA of a mycobacterium in a biological sample, comprising :

- a) a substrate on which a plurality of BAC vectors according to the invention or purified polynucleotides according to the invention have been immobilized;
- b) optionally, the reagents necessary to perform the hybridization reaction.

10       Additionally, the recombinant BAC vectors according to the invention and the polynucleotide inserts contained therein may be used for performing detection methods based on « molecular combing ». Said methods consist in methods for aligning macromolecules, especially DNA and are applied to processes for detecting, for measuring intramolecular distance, for separating and/or for  
15       assaying a macromolecule, especially DNA in a sample.

      These « molecular combing » methods are simple methods, where the triple line S/A/B (meniscus) resulting from the contact between a solvent A and the surface S and a medium B is caused to move on the said surface S, the said macromolecules (i.e. DNA) having a part, especially an end, anchored on the  
20       surface S, the other part, especially the other end, being in solution in the solvent A. These methods are particularly fully described in the PCT Application n° PCT/FR 95/00165 filed on February 11, 1994 (Bensimon et al.).

      When performing the « molecular combing » method with the recombinant BAC vectors according to the inventions or their polynucleotide inserts, the  
25       latters may be immobilized (« anchored ») on a suitable substrate and aligned as described in the PCT Application n° PCT/FR 95/00165, the whole teachings of this PCT Application being hereby incorporated by reference. Then, polynucleotides to be tested, preferably under the form of radioactively or non radioactively labeled polynucleotides, that may consist of fragments of genomic  
30       DNA, cDNA etc. are brought into contact with the previously aligned polynucleotides according to the present invention and then their hybridization position on the aligned DNA molecules is determined using any suitable means including a microscope or a suitable camera device.

      Thus, the present invention is also directed to a method for the detection  
35       of the presence of a polynucleotide of mycobacterial origin in a biological sample

and/or for physical mapping of a polynucleotide on a genomic DNA, said method comprising :

- a) aligning at least one polynucleotide contained in a recombinant BAC vector according to the invention on the surface of a substrate;
- 5 b) bringing into contact at least one polynucleotide to be tested with the substrate on which the at least one polynucleotide of step a) has been aligned;
- c) detecting the presence and/or the location of the tested polynucleotide on the at least one aligned polynucleotide of step a).

The invention finally provides for a kit for performing the above method, comprising :

- a) a substrate whose surface has at least one polynucleotide contained in a recombinant BAC vector according to the invention;
- b) optionally, reagents necessary for labeling DNA;
- 15 c) optionally, reagents necessary for performing a hybridization reaction.

In conclusion, it may be underlined that the alliance of such BAC-based approaches such as described in the present specification to the advances in comparative genomics by the availability of an increased number of complete genomes, and the rapid increase of well-characterized gene products in the public databases, will allow the one skilled in the art an exhaustive analysis of the mycobacterial genome.

## MATERIALS AND METHODS

**1. DNA-preparation.** Preparation of *M. tuberculosis* H37Rv DNA in agarose plugs was conducted as previously described (Canard et al., 1989; Philipp et al., 25 1996b). Plugs were stored in 0.2 M EDTA at 4°C and washed 3 times in 0.1% Triton X-100 buffer prior to use.

**2. BAC vector preparation.** pBeloBAC11 was kindly provided by Dr. Shizuya, Department of Biology, California Institute of Technology (Pasadena, CA). The preparation followed the description of Woo et al., 1994 (Woo et al., 1994).

**3. Partial digestion with *HindIII*.** Partial digestion was carried out on plugs, each containing approximately 10 µg of high molecular weight DNA, after three one hour equilibration steps in 50 ml of *HindIII* 1X digestion buffer (Boehringer Mannheim, Mannheim, Germany) plus 0.1% Triton X-100. The buffer was then removed and replaced by 1ml/plug of ice-cold *HindIII* enzyme buffer containing 35 20 units of *HindIII* (Boehringer). After two hours incubation on ice, the plugs

were transferred to a 37°C water bath for 30 minutes. Digestions were stopped by adding 500 µl of 50 mM EDTA (pH 8.0).

4. **Size selection.** The partially digested DNA was subjected to contour-clamped homogenous electric field (CHEF) electrophoresis on a 1% agarose gel using a BioRad DR III apparatus (BioRad, Hercules, CA) in 1X TAE buffer at 13°C, with a ramp from 3 to 15 seconds at 6 V/cm for 16 hours. Agarose slices from 25 to 75 kb, 75 to 120 kb and 120 to 180 kb were excised from the gel and stored in TE at 4°C.

5. **Ligation and transformation.** Agarose-slices containing fractions from 25 to 75 kb, 75 to 120 kb and 120 to 180 kb were melted at 65°C for 10 minutes and digested with Gelase (Epicentre Technologies, Madison, WI), using 1 unit per 100 µl gel-slice. 25-100 ng of the size-selected DNA was then ligated to 10 ng of *Hind*III digested, dephosphorylated pBeloBAC11 in a 1:10 molar ratio using 10 units of T4 DNA ligase (New England Biolabs, Beverly, MA) at 16°C for 20 hours. Ligation mixtures were heated at 65°C for 15 minutes, then drop-dialysed against TE using Millipore VS 0.025 mM membranes (Millipore, Bedford, MA). Fresh electrocompetent *E. coli* DH10B cells (Sheng et al., 1995) were harvested from 200 ml of a mid-log (OD<sub>550</sub>=0.5) culture grown in SOB medium. Cells were washed three times in ice-cold water, and finally resuspended in ice-cold water to a cell density of 10<sup>11</sup> cells/ml (OD<sub>550</sub>=150). 1 µl of the ligation-mix was used for electroporation of 30 µl of electrocompetent DH10B *E. coli* using a Eurogentec Easyject Plus electroporator (Eurogentec, Seraing, Belgium), with settings of 2.5 kV, 25 µF, and 99 Ω, in 2 mm wide electroporation cuvettes. After electroporation, cells were resuspended in 600 µl of SOC medium, allowed to recover for 45 minutes at 37°C with gentle shaking, and then plated on LB agar containing 12.5 µg/ml chloramphenicol (CM), 50 µg/ml X-gal, and 25 µg/ml IPTG. The plates were incubated overnight and recombinants (white colonies) were picked manually to 96 well plates. Each clone was inoculated 3 times (2 X 200 µl and 1 X 100 µl of 2YT/12.5 µg/ml CM per clone) and incubated overnight. One of the microtiter plates, containing 100 µl culture per well, was maintained as a master plate at -80°C after 100 ml of 80% glycerol were added to each well, while minipreps (Sambrook et al., 1989) were prepared from the remaining two plates to check for the presence of inserts. Clones containing inserts were then designated "Rv" clones, repicked from the master plate to a second set of plates for storage of the library at -80°C.

6. **Preparation of DNA for sizing, direct sequencing and comparative genomics.** A modified Birnboim and Doly protocol (Birnboim et al., 1979) was used for extraction of plasmid DNA for sequencing purposes. Each Rv clone was inoculated into a 50 ml Falcon polypropylene tube containing 40 ml of 2YT medium with 12.5 µg/ml of CM and grown overnight at 37°C with shaking. Cells were harvested by centrifugation and stored at -20°C. The frozen pellet was resuspended in 4 ml of Solution A (50 mM glucose, 10 mM EDTA, 25 mM Tris, pH 8.0) and 4 ml of freshly prepared solution B (0.2 M NaOH, 0.2% SDS) was then added. The solution was gently mixed and kept at room temperature for 5 minutes before adding 4 ml of ice-cold solution C (3M Sodium Acetate, pH 4.7). Tubes were kept on ice for 15 min, and centrifuged at 10,000 rpm for 15 min. After isopropanol precipitation, the DNA pellet was dissolved in 600 µl RNase solution (15 mM Tris HCl pH 8.0, 10 µg/ml RNase A). After 30 minutes at 37°C the DNA solution was extracted with chloroform:isoamylalcohol (24:1) and precipitated from the aqueous phase using isopropanol. The DNA pellet was then rinsed with 70% ethanol, air-dried and dissolved in 30 µl distilled water. In general, DNA prepared by this method was clean and concentrated enough to give good quality results by automatic sequencing (at least 300 bp of sequence). For a few DNA preparations, an additional polyethylene glycol (PEG) precipitation step was necessary, which was performed as follows. The 30 µl of DNA solution were diluted to 64µl, mixed gently and precipitated using 16 µl 4M NaCl and 80 µl of 13% PEG 8000. After 30 min on ice the tubes were centrifuged at 4°C, the pellet carefully rinsed with 70% ethanol, air-dried and diluted in 20 µl of distilled water.
7. **Sizing of inserts.** Insert sizes were determined by pulsed-field gel electrophoresis (PFGE) after cleavage with *DraI* (Promega). 100-200 ng of DNA was *DraI*-cleaved in 20 µl total reaction volume, following the manufacturer's recommendations, then loaded onto a 1% agarose gel and migrated using a pulse of 4 s for 15 h at 6.25 V/cm at 10°C on an LKB-Pharmacia CHEF apparatus. Mid-range and low-range PFGE markers (New England Biolabs) were used as size standards. Insert sizes were estimated after ethidium bromide staining of gels.
8. **Direct sequencing.** For each sequencing reaction 7 µl BAC DNA (300-500ng), 2 µl primer (2 µM), 8 µl reaction mix of the *Taq* DyeDeoxy Terminator cycle sequencing kit (Applied Biosystems) and 3 µl distilled water were used.

After 26 cycles (96°C for 30 sec; 56°C for 15 sec; 60°C for 4 min) in a thermocycler (MJ-research Inc., Watertown, MA) DNA was precipitated using 70 µl of 70% ethanol/0.5 mM MgCl<sub>2</sub>, centrifuged, rinsed with 70% ethanol, dried and dissolved in 2 µl of formamide/EDTA buffer. SP6 and T7 samples of 32 BAC clones were loaded onto 64 lane, 6% polyacrylamide gels and electrophoresis was performed on a Model 373A automatic DNA sequencer (Applied Biosystems) for 12 to 16 hours. The sequences of oligonucleotides used as primers are shown in Table 1.

**9. DOP-PCR.** As an alternate procedure we used partially degenerate oligonucleotides in combination with vector-specific (SP6 or T7) primers to amplify insert ends of BAC clones, following a previously published protocol for P1 clones (Liu et al., 1995). The degenerate primers Deg2, Deg3, Deg4, Deg6 (Table 1) gave the best results for selected amplification of insert termini.

**Table 1: Primers used for PCRs and sequencing**

Vector specific Primers for DOP PCR- first amplification step:

SP6-BAC1: AGT TAG CTC ACT CAT TAG GCA

T7-BAC1 : GGA TGT GCT GCA AGG CGA TTA

Vector specific Primers (direct sequencing, nested primer for second PCR step)

SP6 Mid: AAA CAG CTA TGA CCA TGA TTA CGC CAA

T7-Belo2: TCC TCT AGA GTC GAC CTG CAG GCA

Degenerate Primers:

Deg2: TCT AGA NNN NNN TCC GGC

Deg3: TCT AGA NNN NNN GGG CCC

Deg4: CGT TTA AAN NNN NWA GGC CG

Deg6: GGT ACT AGT NNN NNW TCC GGC

Primers used for the amplification of *M. bovis* DNA in polymorphic chromosomal region of Rv58:

Primer 1: ACG ACC TCA TAT TCC GAA TCC C

Primer 2: GCA TCT GTT GAG TAC GCA CTT CC

**10. Screening by pooled PCR.** To identify particular clones in the library which could not be detected by random end-sequencing of the 400 BAC clones, PCR-screening of DNA pools was performed. Primers were designed for regions of the chromosome where no BAC coverage was apparent using cosmid-or H37Rv

whole genome shotgun sequences. Primers were designed to amplify approximately 400-500 bp. Ninety-six-well plates containing 200  $\mu$ l 2YT/12.5  $\mu$ g/ml CM per well were inoculated with 5  $\mu$ l of -80°C glycerol stock cultures each from the master plates and incubated overnight. The 96 clones of each plate were pooled by taking 20  $\mu$ l of culture from each well and this procedure was repeated for 31 plates. Pooled cultures were centrifuged, the pellets were resuspended in sterile water, boiled for 5 minutes, centrifuged and the supernatants kept for PCRs. As an initial screening step, the 31 pools of a total of 2976 BACs, representing about two thirds of the library were tested for the presence of a specific clone using appropriate PCR primers. PCR was performed using 10  $\mu$ l of supernatant, 5  $\mu$ l of assay buffer (100 mM b-mercaptoethanol, 600 mM Tris HCl (pH 8.8), 20 mM  $MgCl_2$ , 170 mM  $(NH_4)_2SO_4$ ), 5  $\mu$ l of Dimethylsulfoxide (DMSO), 5  $\mu$ l of dNTPs (20 mM), 5  $\mu$ l of water, 10  $\mu$ l primer (2  $\mu$ M), 10  $\mu$ l inverse primer (2  $\mu$ M) and 0.2 units of *Taq* DNA polymerase (Boehringer). 32 cycles of PCR (95°C for 30 s, 55°C for 1 min 30 s, 72°C for 2 min) were performed after an initial denaturation at 95°C for 1 min. An extension step at 72 °C for 5 min finished the PCR. If a pool of 96 clones yielded an appropriate PCR product (Fig. 1A), subpools were made to identify the specific clone. Subpools representative for lane A of a 96 well plate were made by pooling clones 1 to 12 from lane A into a separate tube. Subpools for lanes B to H were made in the same way. In addition, subpools of each of the 12 rows (containing 8 clones each) were made, so that for one 96 well plate, 20 subpools were obtained. PCR with these 20 subpools identified the specific clone (Fig. 1B, lower gel portion). If more than one specific clone was present among the 96 clones of one plate (Fig. 1B, upper gel portion), additional PCR reactions had to be performed with the possible candidates (data not shown).

**11. Genomic comparisons.** DNA from the BAC clone Rv58 was digested with the restriction endonucleases *Eco*RI and *Pvu*II, and resolved by agarose gel electrophoresis at low voltage overnight (1.5 V/cm). DNA was transferred via the method of Southern to nitrocellulose membranes (Hybond C extra, Amersham) following standard protocols (Sambrook et al., 1989), then fixed to the membranes at 80°C for 2 hours. The blot was hybridized with  $^{32}P$  labelled total genomic DNA from *M. tuberculosis* H37Rv, *M. bovis* type strain (ATCC 19210) or *M. bovis* BCG Pasteur. Hybridization was performed at 37°C overnight in

50% formamide hybridization buffer as previously described (Philipp et al., 1996b). Results were interpreted from the autoradiograms.

12. **Computer analysis.** Sequence data from the automated sequencer ABI373A were transferred as binary data to a Digital Alpha 200 station or Sun SparcII station and analysed using TED, a sequence analysis program from the Staden software package (Dear et al., 1991). Proof-read sequences were compared using the BLAST programs (Altschul et al., 1990) to the *M. tuberculosis* H37Rv sequence databases of the Sanger Centre, containing the collected cosmid sequences (TB.dbs) and whole-genome shotgun reads (TB\_shotgun\_all.dbs) (http://www.sanger.ac.uk/). In addition, local databases containing 1520 cosmid end-sequences and the accumulating BAC end-sequences were used to determine the exact location of end-sequenced BACs on the physical and genetic map. MycDB (Bergh et al., 1994) and public databases (EMBL, Genbank) were also used to compare new sequences, but to a lesser extent. The organization of the open reading frames (ORFs) in the polymorphic region of clone Rv58 was determined using the DIANA software established at the Sanger Centre.

## EXAMPLES

Example 1 : Construction of a pBeloBAC11 library of *M. tuberculosis* H37Rv.

Partial *Hind*III fragments of H37Rv DNA in the size range of 25 to 180 kb were ligated into pBeloBAC11 and electroporated into strain *E. coli* DH10B. While cloning of fractions I (25 to 75 kb) and II (75 to 120 kb) gave approximately  $4 \times 10^4$  transformants (white colonies), cloning of fraction III (120 to 180 kb) repeatedly resulted in empty clones. Parallel cloning experiments using partial *Hind*III digests of human DNA resulted in stable inserts for all three fractions (data not shown), suggesting that the maximum size of large inserts in BAC clones is strongly dependent on the source of the DNA. Analysis of the clones for the presence of inserts revealed that 70 % of the clones had an insert of the appropriate size while the remaining 30% of white colonies represented empty or *lacZ'*-mutated clones. Size determination of randomly selected, *Dra*I-cleaved BACs via PFGE showed that the insert sizes ranged for the majority of the clones between 40 kb and 100 kb with an average size of 70 kb. Clones with inserts of appropriate size were designated with "Rv" numbers, recultured and stored at -80°C for further use.

**Example 2 : Direct DNA sequence analysis of BACs.**

To characterize the BAC clones, they were systematically subjected to insert termini sequencing. Two approaches, direct sequencing of BAC DNA and PCR with degenerate oligonucleotide primers (DOP), adapted to the high G+C content of mycobacterial DNA, were used. In a first screening phase, 50 BAC clones designated Rv1 to Rv50 were analysed using both methods in parallel. Except for two clones, where the sequences diverged significantly, the sequences obtained by the two methods only differed in length. Sequences obtained directly were on average about 350 bp long and for 95% of the clones both the SP6 and T7 end-sequences were obtained at the first attempt. Sequences obtained by DOP-PCR were mostly shorter than 300 bp. For 40% of the BACs we obtained only very short amplicons of 50 to 100 base pairs from one end. In two cases the sequence obtained with the DOP-PCR differed from the sequences obtained by direct sequencing, and in these cases *E.coli* or vector sequences were amplified (data not shown). Taking the advantages and disadvantages of both methods into account, we decided to use direct termini sequencing for the systematic determination of the SP6 and T7 end-sequences.

**Example 3 : Representativity of the library.**

After having determined the end-sequences of 400 BACs a certain redundancy was seen. The majority of clones were represented at least 3 to 4 times. Maximum redundancy was seen in the vicinity of the unique *rrn* operon, as 2.5 % of the clones carried identical fragments that bridge the cosmids Y50 and Y130 (Fig. 3, approximate position at 1440 kb). The majority of clones with identical inserts appeared as two variants, corresponding to both possible orientations of the *HindIII* fragment in pBeloBAC11. This suggests that the redundancy was not the result of amplification during library construction, but due to the limited number of possible combinations of partial *HindIII* fragments in the given size-range of 25 to 120 kb. To detect rare BAC clones, a pooled PCR protocol was used. Primers were designed on the basis of the existing cosmid sequences and used to screen 31 pools of 96 BAC clones. When positive PCR products of the correct size were obtained, smaller subpools (of 8 or 12 clones each) of the corresponding pool were subsequently used to identify the corresponding clone (Figs. 1A and 1B). With this approach 20 additional BACs (Rv401-Rv420) were found for the regions where no BACs were found with the initial systematic sequencing approach. The end-sequences of these BACs

(Rv401-420) were determined by direct sequencing, which confirmed the predicted location of the clones on the chromosome. A 97% coverage of the genome of H37Rv with BAC clones was obtained. Only one region of ~ 150 kb was apparently not represented in the BAC library as screening of all pools with several sets of specific primers did not reveal the corresponding clone. This was probably due to the fact that *HindIII* fragments of mycobacterial DNA larger than 110 kb are very difficult to establish in *E. coli* and that a *HindIII* fragment of ~120 kb is present in this region of the chromosome (data not shown).

#### Example 4 : Establishing a BAC map.

Using all end-sequence and shotgun-sequence data from the H37Rv genome sequencing project, most of the BAC clones could then be localized by sequence comparison on the integrated map of the chromosome of *M. tuberculosis* strain H37Rv (Philipp et al., 1996b) and an ordered physical map of the BAC-clones was established. PCR with primers from the termini sequences of selected BACs were used for chromosomal walking and confirmation of overlapping BACs (data not shown). The correct order of BACs on the map was also confirmed more recently, using 40,000 whole genome shotgun reads established at the Sanger Centre. In addition, pulsed-field gel electrophoresis of *DraI* digests of selected BACs was performed (Fig. 2) in order to see if the approximate fragment size and the presence or absence of *DraI* cleavage sites in the insert were consistent with the location of the BACs on the physical map (Fig. 3). Comparison of the sequence-based BAC-map with the physical and genetic map, established by PFGE and hybridization experiments (Philipp et al., 1996b), showed that the two maps were in good agreement. The positions of 8 genetic markers previously shown on the physical and genetic map were directly confirmed by BAC-end-sequence data (Table 2, Fig. 3). The position of 43 from 47 Y-clones (91%) shown on the physical and genetic map, which were later shotgun sequenced, was confirmed by the BAC end-sequences and shotgun sequence data. Four clones (Y63, Y180, Y251, and Y253) were located to different positions than previously thought and this was found to be due to book keeping errors or to chimeric inserts. Their present approximate location relative to the *oriC* is shown in Figure 3: Y63 at 380 kb, Y63A at 2300 kb, Y180 at 2160 kb, Y251 at 100 kb, and Y253 at 2700 kb. A total of 48 BACs, covering regions of the chromosome, not represented by cosmids were then shotgun sequenced (Cole et al., 1997), and these are squared in Fig. 3. No chimeric BACs

were found, which is consistent with the observations of other research groups for other BAC libraries (Cai et al., 1995; Zimmer et al., 1997). The absence of chimeric BACs was of particular importance for the correct assembly of the *M. tuberculosis* H37Rv sequence. The exact position of the BAC termini sequences  
 5 on the chromosome will be available via the world wide web (<http://www.pasteur.fr/MycDB>).

Table 2 : Identities of genetic markers previously shown on the integrated and genetic map of H37Rv (Phlipp et al., 1996b) wich showed perfect sequence  
 10 homology with BAC ens sequences.

Locus	BAC end sequence	Description of genetic marker	Organism	GenBank Accession n°
<i>apa</i>	Rv163SP6	Secreted alanine-proline-rich antigen	<i>M. tuberculosis</i>	X80268
<i>dnaJ, dnaK</i>	Rv164T7	DnaJ hsp	<i>M. leprae</i>	M95576
<i>fop-A</i>	Rv136T7	Fibronectin binding protein	<i>M. tuberculosis</i>	M27016
<i>polA</i>	Rv401T7	DNA polymerase I	<i>M. tuberculosis</i>	L11920
<i>ponA</i>	Rv273T7	Penicillin binding protein	<i>M. leprae</i>	S82044
<i>psiC</i>	Rv103T7	Putative phosphate transport receptor	<i>M. tuberculosis</i>	Z48057
<i>recA</i>	Rv415SP6	Homologous recombination	<i>M. tuberculosis</i>	X58485
<i>wag9</i>	Rv35SP6	35-kDa antigen	<i>M. tuberculosis</i>	M69187

#### Example 5 : Repetitive end-sequences.

Repetitive sequences can seriously confound mapping and sequence  
 15 assembly. In the case of the BAC end-sequences, no particular problems with repetitive sequences were observed. Although nine clones with one end in an *IS1081* (Collins et al., 1991) sequence were identified, it was possible to correctly locate their position on the map using the sequence of the second terminus. Moreover, these BACs were used to determine the exact locations of  
 20 *IS1081* sequences on the map. Five copies of this insertion sequence, which

harbors a *Hind*III cleavage site, were mapped on the previous physical and genetic map. In contrast, BAC end-sequence data revealed an additional copy of *IS1081* on the *M. tuberculosis* H37Rv chromosome. The additional copy was identified by six clones (Rv27, Rv118, Rv142, Rv160, Rv190, Rv371) which  
5 harbored an identical fragment linking Y50 to I364 (Fig. 3, at ~ 1380 kb). This copy of *IS1081* was not found by previous hybridization experiments probably because it is located near another copy of *IS1081*, localized on the same *Dra*I fragment Z7 and *Asn*I fragment U (Fig. 3, at ~ 1140 kb). Furthermore, the position of a copy of *IS1081* previously shown in *Dra*I fragment Y1 (Fig. 3, at  
10 ~ 1840 kb) had to be changed to the region of Y349 (Fig. 3, at ~ 3340 kb) according to the end-sequences of BAC Rv223. The positions of the four other *IS1081* copies were confirmed by the sequence data and therefore remained unchanged. In total 6 copies of *IS1081* were identified in the H37Rv genome in agreement with the findings of others (Collins et al., 1991).

15 In addition, a sequence of 1165 bp in length containing a *Hind*III site was found in two copies in the genome of H37Rv in different regions. The end-sequences of BAC clones Rv48 and Rv374, covering cosmid Y164, as well as Rv419 and Rv45, that cover cosmid Y92, had perfect identity with the corresponding parts of this 1165 bp sequence (Fig. 3, at ~ 3480 kb and ~ 900 kb).  
20 Analysis of the sequence did not reveal any homology with insertion sequences or other repetitive elements. However, as each of the two locations showed appropriate BAC coverage, chimerism of the sequenced cosmids Y164 and Y92 can be ruled out as the probable cause.

#### Example 6 : Using BAC clones in comparative genomics.

25 The minimal overlapping set of BAC clones represents a powerful tool for comparative genomics. For example, with each BAC clone containing on average an insert of 70 kb, it should be possible to cover a 1Mb section of the chromosome with 15 BAC clones. Restriction digests of overlapping clones can then be blotted to membranes, and probed with radiolabelled total genomic DNA  
30 from, for example, *M. bovis* BCG Pasteur. Restriction fragments that fail to hybridize with the *M. bovis* BCG Pasteur DNA must be absent from its genome, hence identifying polymorphic regions between *M. bovis* BCG Pasteur and *M. tuberculosis* H37Rv. The results of such an analysis with clone Rv58 (Fig. 3, at ~1680 kb) are shown here. This clone covers a previously described polymorphic  
35 genomic region between *M. tuberculosis* and *M. bovis* BCG strains (Philipp et

al., 1996a). *Eco*RI and *Pvu*II digests from clone Rv58, fixed on nitrocellulose membranes, were hybridized with <sup>32</sup>P-labelled total genomic DNA from *M. tuberculosis* H37Rv, *M. bovis* (ATCC 19120), and *M. bovis* BCG Pasteur. Figures 4A and 4B present the results of this analysis, where it is clear that several restriction fragments from clone Rv58 failed to hybridize with genomic DNA from either *M. bovis* or *M. bovis* BCG Pasteur. On the basis of the various missing restriction fragments, a restriction map of the polymorphic region was established and compared to the H37Rv sequence data. The localization of the polymorphism could therefore be estimated, and appropriate oligonucleotide primers (Table 1) were selected for the amplification and sequencing of the corresponding region in *M. bovis*. The alignment of *M. bovis* and *M. tuberculosis* H37Rv sequences showed that 12,732 bp were absent from the chromosomal region of the *M. bovis* type strain and *M. bovis* BCG Pasteur strain. The G+C content of the polymorphic region is 62.3 mol%, which is the same as the average genome G+C content of the *M. tuberculosis* genome, hence indicating that this region is not a prophage or other such insertion. Subsequent PCR studies revealed that this segment was also absent from the Danish, Russian, and Glaxo substrains of *M. bovis* BCG, suggesting that this polymorphism can be used to distinguish *M. bovis* from *M. tuberculosis*. Analysis of this sequence showed that 11 putative open reading frames (ORFs) are present in *M. tuberculosis*, corresponding to ORFs MTCY277.28 to MTCY277.38 / accession number Z79701 -EMBL Nucleotide Sequence Data Library (Fig. 5). FASTA searches against the protein and nucleic acid databases revealed that the genes of this region may be involved in polysaccharide biosynthesis. Among these putative genes, the highest score was seen with ORF 6 (MTCY277.33), whose putative product shows a 51.9% identity with GDP-D-Mannose dehydratase from *Pseudomonas aeruginosa* (accession number U18320 - EMBL Nucleotide Sequence Data Library) in a 320 amino acid overlap. The novel *M. bovis* sequence of the polymorphic region was deposited under accession number AJ003103 in the EMBL Nucleotide Sequence Data Library.

As it appears from the teachings of the specification, the invention is not limited in scope to one or several of the above detailed embodiments; the present invention also embraces all the alternatives that can be performed by one skilled in the same technical field, without deviating from the subject or from the scope of the instant invention.



## Clone Rv104

.....Rv104SP6.seq:.....  
ATACTCAAGCTTTGCCGACGAGCGGGCGATGTTGATGACGGGAAACCCAGCGCACAAACCGACGATTTTGGCGTAGCC  
GGCGGACGTCTGCTCGATTCCGATCACGTGCGCGCTCGCATCGAGCATGGCGCCGGCGACGGCTAGCAGCGATCCGCC  
GTCGTGAGGAGCACGACACGAGCCGTACGCCCCGGCCGTAAGCCGCGCCAGGATTCGGCGAAAAACCGTTCTACGTG  
GCGGGTGTACTGGGTGTCGAATGATTGCGTGGGGTGCCTAGGCGTCTGCAATCGTCGACATAGATGCCGTGCGGGCCG  
CATCGCGTCGACAACTCCGGGTGAGTGGAATAGCACTTGCCGATCACCGCGACGTTGCGCGGATGAGGCCGAACCCGA  
ATA

.....Rv104T7.seq:.....  
TCCTATGTCCCTGCCGAGCANGTGATCGAACGCGGTGACAGATTTGTCTATCCTGGACCTGACGGTGAGGTCGAAGTT  
TTCCAGGAATTCGGCAAAATCGGTAAGAGCCTGAAGAATTGCGTATCGCCGGACGAAATCTGCGACGCATACGGGGGC  
ATATACGCTTCGGGTTTACGAGATGTCGATGGGGCCGCTGGAGGCTTACGTCCATGGGCCACAAAGGATGTTGTCGG  
CGCGTACCGTTTTCTGCAGCGGGTGTGGCGCTTGCTCG

## Clone Rv105

.....Rv105SP6.seq:.....  
ATACTCAAGCTTGATTCGCCGAAACCGACCGTGAGCACCCCGCCAGCCACCACGCTCGGGTCGGGCGCCGGGCCCGG  
GCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCACCGGCTGCGCTACGTCTAACCATTCCAGGCG  
GAGCTACATCAGCTCGGCCGCCAGTGTTCGGGCCCTCTTCCAGGTCGAAGTCTATACCGATATGCGCATCCGCAGC  
CGCCACCCCTGGAGAACAGACGATGCCCTACTAATGCTTGTCTGGCGGGGCC

.....Rv105T7.seq:.....  
GGTACGCTTCGGTCGCGAGTCTGCGAGTGATGCATGACGACCGGGACCTCGTCGGCATCTTCCATAGCCCGCCACACCT  
TCAGTTGCTCACCGGAATCCAACCGGTAGAAGGTGCGCGAGCGCTCGGCATTGGTCATCGGGATATGCCGCTCGGGAC  
GGTCAGAGCCCTCGGGTCCGGCCAGCACTCCGCAGGCTTCGTGCGGGTGGTCGCGACGCGCATGGGCCACCATCGCAT  
TCACCAGGTCTGCGCAATCACCAGCACGTAGACGGTTCTTTTCTAAGCAACACCGAAGTTTCAGGACCCGAATGCT  
CCGGGAAACATGTCACGGTAGGTGCGTATTCCGGCTACCGGCTGA

## Clone Rv106

.....Rv106SP6.seq:.....  
GGCGTCAACGGTGTGGAACCCGCGTCAAGCAATTGGTAGGCCTGCAGTCTGTGAATCAGGCCGACGCTGTGGCCGCC  
GCGGC

.....Rv106T7.seq:.....  
GGCTNGCGTACCCGGTACCGGCCGCGGGCTACCACGTGCCGGAAGTGAAGCGCAGTAAGCCCTCAACGCGCCACCG  
CTTTGGCCCGCGCGCCGGCTAGGCGCATCGGCGGTGGCCGTGGGCGGCGCACTGCGACCTCACCAGCGGCTTTCG  
AGCTTTGTTGATCAACCGGCCAGCATGGTCGANGATGCATTGAGACCATATTGAAATTGGTTTCATCGGGGGCCC  
CGATCCGATGCCCCCTCCAGTTGCGTGAGCAANCAGCGGAGTCNTCGCGGGATCGATGGCCACGGGGTGTTCATGG  
CGGATGGTCCGCTGCCCGCGCACTGGCTCTTGCGGGAGAACCGATCTAGCACCACCGATCCGCGCACGTNG

## Clone Rv107

.....Rv107T7D4.seq:.....  
CGTAATNTCGCGCACANCCANGACTTCTGGGGGGATCNGCTGACAGTGGTNGGATCCCAAATTGCGGATGATCGGGCC  
GCCNACGTGCTTGTGTACCTCNTCNGTCACAACNAANCCGAANCATGACTCGGTCCACGCGGTGCGGCACATGGTG  
GACACCACACCGCCACCGCNCGGGTGAAGGCCTATGTACCCGGTCCGGCAACACTCAATGCCGACCAGGCCGANGCC  
GGACACNANAGTATCNCTAACGTACCGCGATCACGAGCATGGTGATCGNNCAATGTTNCTANTGATCTATCGCTCCG  
TAATTACCGCGGTTCTCGTCTTGATCATGGTCGCANCGAACTCCGGCGCAATCCGCGGATTTCATCGNCTTGCTCGCCG  
ATCACAATTTTACGCCTTTACATTGCAACNAACCTGCTCGTCTCATGGNGATGCGGCGACACGGACTACCGATATC  
ATGCTCGCCGTTACACAATCNCGCCACGCCGCGAAGACNGGAAACGCTTCTACACAATNTTNCGGGACGCCACTNAA  
CTTGGTTCNGGTTTGACATTGCCGCGCATGTNTGCCAGCTTTGCCGGCTCCCTTA

## Clone Rv108

.....Rv108T7D4.seq:.....  
TGAATTTCCCGATCCCAATCTCGGTTAGATACAGTTCGCCATACCCCTTACTTCGGCAACGCTGGGCGGATTGGC  
CCTGCNGCTGCAGCANACCATCGACGCCATCGAATTGCCGGCAATCTCGTTAGCCAATCCATACCCATCGACATTCC  
GCCGATCGACATCCCGGCCCTTCNCCCTTTAACGG

## Clone Rv109

:::Rv109SP6.seq:::

AACAGCTATGACCATGNTTACGCCAAGCTATTTAGGTAACACTATANAATACTCAAGCTTTTACGGTGATCGCGCATC  
ACCTGGTTCATGAACGGAAGCAGCGCANCCTTCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCCGCGGTCNCG  
TGCAGGTGCTCGGGCAGCTCGGCCCGGACAGCCGCCTGACCCTGAAACCAGCTTCCATATCCCGCGACNAACNACNCC  
AGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCGTTCTCCACCGACCGGGCCCGGGTGTGGGGTGT  
TTCGGCGACCGGCAGCCAGGTGGTCCACACTGCCGACGGGCGCCGCGAGCCGTTACCCGACCAAGCCGCCGAACAAGT  
CCGCCGATCGCATACTCCAACCGTTGCGGTACTGCGAGTCACTGGCGTACCTCCTCNCGCTCGGCGAAGTCT  
TGCTCCANCACGTGCGAGAACGGCAAGGAACACGTTCA

:::Rv109T7.seq:::

GACCGNCCATGTTTCCACAATGTGGTGCCAGTNCGGNGGCTACGTGCCATCNANACACTGGCGCAGGCTATCGCACC  
CGTTATCNGCTACGAACAAATCNCGGTATGCGTTCTTTANCATGAGTCGGCGACCGNCGATCATGGTCGACACCCACG  
ACNGAAATACGCAGATCGCCNTCNAAGTGTGTGCCGCGGATTATCANGACTGACCTCCTGGCTGACCGGNNGTGNTG  
GTCCGATGCTTGGCGCCCGCGCGGTGNTCGTGGTCGGCTCGGATAGCGAAGTCAGCTAATTCTCGTGGCAGCTCG  
AAAGGTCCTGCCGGTGCCGGTCTTTGCGCAAACCATGCNCATGTTACGGTCCCTCGGGTGGCGCCTGGCGGCGGC

## Clone Rv10

:::Rv10SP6D2.seq:::

GGGATGGGCGGGCCGCTAAACTCTTCGTGTTCCACTAACTCCGGGAGGGNCAATCTCGGGCCGTATGGCTCACGTC  
GCGTCGCCCTCCGACCGCAACATTCGGAGTTGGCAGCAACCTGGTAGCACCCCTGGCCGG

:::Rv10T7D4.seq:::

NCCGTCGTTGACAAGTAAATATGTCCGCAAAAGTCTCAGCGGCCGACTTTGCTCGCAGGTGGCGGTACCGCGCCACCG  
AGTCGATGCCGTGGTCGCGGAAGATGCCTCCCGAAATCGCACGGCCTTCCCNNTTTAAACGGA

## Clone Rv110

:::Rv110SP6.seq:::

TTTAGGTGACACTATAGAATACTCAAGCTTTTGGTCTAGCCGGCCGAGCAGATACGGGTGTCAATTGGCCACCGGCGG  
CGGCTGTCCGGGAAATGGCGGGTCCCCGGTGGTTTTGCTGATGAGTGCTGAACCGTANTCGAAGTGGGCGGCGTCAGA  
CTCCACCCANCCAGCAGGCAGCGGAAGCTGAATCCTCCAACCGGGTTGTGNATCCGGACAAGTTGGGGTGCCTTTGG  
GGCAATGACAGGTGGCNGCGGTGCGTTCGGGTCCGCCGCGGAAGTGCTGCGTTGGGATCNCCTGGTGGGCATTTCGGC  
NTTTTTGCGGCGGCGGTGGTNGGGGGCAACAGGTNTCCNNGTGCGGGTGGCGCTCAACGGTCNACGGCGCAAGCCG  
CCGTTGTTGGTACCNGGGGCGCTGGCTCCGGATCGCGTTGGCGGTCNCCGG

:::Rv110T7.seq:::

CTACACCATCGAATACGACGGCGTCGCCNACTTTCCGCGGTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGC  
CGGCACCTACTACGTGCACTCCAACCTACTTCATCCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATAC  
GGTCGGTCCCAGTACCCAGTACTACATCATTCGCACGGANAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCC  
GATCGTGGGGAACCCACTGGCGAACCTGGTTCAACCAAACTTGAANGTGATTGTTAACCTGGGCTACNGCGACCCGGC  
CTATGGTTATTCNACCTCNCGCCCAATGTTGCGACTCCGTTCCGCTTGGTCCANAAGTCNNCCGGTCGTCATCGC  
CGAANCTCTCNCCTCCCGGACCCACAGGAATCNCNATTTCCNCTACAAATCANCCACCTCCA

## Clone Rv111

:::Rv111T7.seq:::

GCATGATCGGCCACCTTTCCGGGCCGCCGGCATAACGGCGGCGTACCGATCTCCGCGTCATACACCCGCGGGTAATCGC  
CGACGGTGCCGGTTCGCGAGCCGAAGGTGACGACTCTGATTGAATCGAGTTCAGGTCCAGCGGGTGGCGCACCAACG  
GCGCGAGCTCAACGACGTCAATCNCGTTGTGCTTTCTACGGTCACCGACCCCTGGTGACCGTAGTTTCNCCC

## Clone Rv112

:::Rv112SP6.seq:::

GACACTATAGAATACTCAAGCTTGCCAACCGCCAGCCTGCATCCGGCGGCGANCACTGCTCCGCCGACCGTACGAAC  
CAACCTGCGGTGCCAGGCCATTGACGATGTGCTGGTCGGCGCCCGGAGTCCGCGCACCATCAACGCCGCGGGCACC  
ACCANGGCGGCCCCACCTGCACGGCGACGATCATTCGGCGCCGCTCACGGCGGGCGGGGCTCGAACANGCACAGCA  
TCAACGTNGTCACCCGGCCGTGACCGGCCGCATCGTCACACCACCCAAAGCCCATTGCCGTCCTCCTCAACNGGGCGA  
CCCCGCCCGCATCGTCACAGGNCCTAAGGCCATTGCCGTCCTCCT

:::Rv112T7.seq:::

TCGGCGCCATCGGCACCTTCGAGGACCTGTATTTTCGACGCCGTGGCCNACCTGAGGTTGGCGGTGGACNAAGTGTGCA  
CCCGGTTGATTTCGCTCGGCCCTTGCCGGATGCCACCCNGCGCTGGTGGTTCGATCCGCNAANAGACAANTTGTGGTGA  
NGCTTCTGCTGCCTGCGACACCCACNACGTGGTGGCACCAGGCGAGCTTTAGCTGGCATGTCCTGACCGCGCTGGCCGA  
CNACTCCAGACNTTCCACNAANGGTGCCNNCCCAATGTNCCGNANTGTCTCCGGNTCCCTTTACCNCCCAATGGGCN  
GNTTCCACNGGTTACGGGGCCCNNTNCCGGCGGGTCTNCCTCCCAANTACCAAATACGCCCCGACNTTCCGGA

## Clone Rv113

:::Rv113SP6.seq:::

ATACTCAAGCTTTTATGGTGATCGCGCATCACCTGGTTCATGAAGTGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCA  
ACATGAGCCAGCCTCTCGTCGGCGGTTCGGGTGCAGGTGCTCGGCCAGCTCGGCCGCGAACAGCCCGGCTTGAACCCGTG  
AAAACNGCTTTCCATATCCCGCGACGAAAGAACGCCAGTTCGGCTACTTAACCCCTCCGCGAACCGTCCATGGACAA  
CAGCGCGTTCTCCACCAACCGGGCCCGGGTGT

:::Rv113T7.seq:::

TCGGCTCAGGCCGCGCTGCTGGTAGAGTCGCTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTTCGGCGGCTACGT  
GCCATCGAGACACTGGCGCAGGCTATCGCACCCGTTATCGGCTACGAAGCAAATCGCGGTATGCGTTCTTGAGCATGA  
GTCGGCGACCGTTCGTTCATGGTCGACACCCACGACGGAAGACGCAGATCGCCGTCAAGCATGTGTGCCGCGGATTATC  
AGGACTGACCTCCTGGCTGACCGGCATGTTTGGTCGCGATGCCCTGGCGCCCGGCGGCGTGGTTCGTGGTTCGGCTCGGA  
TAGCGAGGTCAAGCAATTCGTGGCAGCTCGAAAGGTCTGCCGTTGCCGTTCTTTGCGCAAACAATAGCGCAGGT  
TACGGTTCGCGCGGGGTGCGGCCTGGCGGCGGCC

## Clone Rv114

:::Rv114SP6.seq:::

CAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCGCGTCTACGCCGGCCCGGAGCATCCGCACAGCGCTCAGCA  
GCCGGTTCCGTACGANCTCAAGCAGGTGGCGCAATGACCGAAACCAACCCAGCCCCGCAAACCCCGGCGGCCCGGCC  
GGGCCCCGACAATCGTTTCGTGTTGGAGCGGCCCATCCANACCGTTGGGCGCCGTAAGGANGCCGTGGTACGAATGCGG  
CTGGTGCCCGGCACCGGCAAGTTCGACCTCAACGGCCGCGAGCTTGGANGACTACTTCCCAAACAAGGTGCACCAGCAG  
TTGATCAAGGCACCCCTGGTCACCGTGGATCGGGTGGAAAGTTTCGACATCTTTGCCACCTGGGCGGCGGCGGCCGT  
CCGGTCAGGCCGGGCTGCCCTGGGTATCGCCCGGCATGATTCTGGTATCCCCNGAAGAACCG

:::Rv114T7.seq:::

CGGTTGGCCACCGCTTCTGCGGTGCCCGCGCGTCGACAATGACCGTGTCTCCTTGCTGACCACCACGCGTCGGGCC  
GAGCCCAGCACCTCCAAGCCACCTCGCGCAGCACCATGCCGGCGTCGGGGTTGACCACCTGGCCACCCGTCAACACC  
GCCAGGTCTCAAGGAAACGCCTTACGGCGGTCAACGAAGTACGGCCCTTGACCGCGACCGCTTTCAACGTCTTGCG  
AATCGCGTTGACGACCAGCGTCGCCAACGCTTCGCCCTCCACGTCTTCAGCCACGATCAGTAGTGCTTACCCGTTCC  
TGCAACCTTTTCCAGCAATGGCAACAGATCGGGAAGCGANCTGATCTTGTCTTGGTGCN

## Clone Rv115

:::Rv115SP6.seq:::

CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTTTGGCTGGGTTCGCTTCGAATTCNGCGTGACCCGCTATGG  
GTTGCANCAGCGGTGGCGCCGACACCCCACTGGCCCGGGTGTTCGCCCCGAACCCGGATCATGGTGAGCGAAAA  
GGANATTCNCCTGTTTCGATGCTGGGATTCGCCACGCCAAGGCATCTANCGATTACTCTCCNCGGGGTGGGAAAAGTGC  
CCAATCCCCCTCCCTCCAACCTTCCNAACAATCATTCGGTTCNCCNTCCGGTTGGNGGTAACCNCCAAATAAAACC  
CCTGCCCG

:::Rv115T7.seq:::

GCCCGCNCATGGCCAATCCCCGAAGACATCATTTGGCCAGTGGCCGGGCGCTAACAGGTTCCAGCCCCCACCANTGCC  
GCTCGAACATGCGGTGCAACCCATTTCGAGGCCGGCAGGGAAGACCCGCGGAAGCCGCAAAGGGCTGCAGTTCGCG  
CCCAATAATGTCGTCCGCAACCGATGCGCTCNAAAACCNCCGGCAGTCAGCGCACCCGACGCGANGTCGAAAGAC  
GTCTCAGCGCGGCCACATGGGGTGCCAATCGGCACGGCAGGTATGCCGCGCGCAACCCGAGCGCGTGGTGCATGCC  
ACGGTCCGCGANGGCGCANACCCGCCAATGCCGAANCCACGAAACATCGGGCGCATCCACCTTCAACC

## Clone Rv116

:::Rv116SP6.seq:::

ATACTCAAGCTTGGCCAGCCGTTCGATGACAAGAAATATGTCCGAAAAGACTCAGCGGCCGACTTTGCTCGCAGCTGG  
CGGTACCGCGCCACCGAGTCGATGCCGTGGTTCGCGGAAGAATGCCTCCCGAATTCGCACGGCCAATTCCATTCCGGGA  
AGCATCCGCAATGCCAGTTCGGTTGCCCCCTGCCGGCCACGGCACCCACTTGCGGCATTCGCTCCACCTGGGCCAGC  
GCCCGCGCGCAATTCGAAACAATAAAATTGCACCCGGC

.....Rv116T7.seq:.....

CCACCCGTGTATTTTGGGATGGGCAAAAAGGCGAAGCACCAGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGG  
CTAGGGCTTCTCGCGGGAAGGCCCCGAACGTACGGCGTTTCAACACGTGCGCTCGCCCTCCGACCGCGAACATTTCGGGG  
ATGGCAGCAACCTGGTAGCACCTGGCCGGGCGATGATCTGCAGCGTCGCCCGGGTAGTCGCCCGCCGGGCGGCTAC  
AGTCTGAAACGCGATGACCATCGATGTGTGGATGCAGCATCCGACGCAACGGTTCCTACACGGCGATATGTTTCGCTC  
CCTGCCCCGT

Clone Rv117

.....Rv117SP6D2.seq:.....

CTGCCCATGTTTGGGGACGCCCCGACCAGCCGATGCTGGAGGCCCTACACGGCCCTTGGTGGCTGGCCACGGCGACCGA  
GCGGCTGCAACTGGGCGCGTTGGTGACCGGAATACCTACCGCAGCCNGACCCCTNTCNCAANAGGATNTTGTTCGCC  
GGACCCNCTC

.....Rv117T7D4.seq:.....

CCGACTTTCGCGGTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCA  
ACTTCATCCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACT  
ACATCATTCGCACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAAC  
TGGTCAACCAAACTTGAAGGTGATTGTTAACCTGGGCTACGCGACCGCCTT

Clone Rv118

.....Rv118SP6.seq:.....

ATACTCAAGCTTTGTACACCAAGTGTTCGACCAGGCGCTCCATCCGGCGAGTGGATACTCCCAGCAGGTAGCAGGT  
CGCCACCACGCTGGTCAGTGCGCGTTTCACTCGCTTGC GGCGCTGCAGCAGCCATTTCGGGAAATACCTGCCCTGGCG  
CAGCTGGGGGATCCCAACTTCAATGTTGCGGCACGGGTGTCAAATTCACGGTGGCGGTAGCCGTTGCCCTAATTGGA  
CCGCTCATCGCTGCTTTCGCGGTACCCCGCCCGCACAGGGCTTCGGCTTCAGCCCCCATCAGGGCGGCAATAAACTT  
CAAGAGCACC

.....Rv118T7.seq:.....

GAGGCAGCTTCGCCGGCAATTCTACTAGCGAGAAGTCTGGCCCCGATACGGATCTGACCGAAGTCGCTGCGGTGCAGCC  
CACCCTCATTGGCGATGGCGCCGACGATGGCGCCTGGACCGATCTTGTGCCGCTTGCCGACGGCGACGCGGTAGGTGG  
TCAAGTCCGCTTACGCTTGGGCCTTTGCGGACGGTCCCGACGCTGGTTCGCGGTGCGCCGCGAAAGCGGCGGGTCGG  
GTGCCATCAGGAATGCCTCACCGCCGCGGCACTGCACGGCCAGTGCCGCGCGATGTACGCCATCGGGACATCATGCT  
CGCGTTCATACTCCTCGACCAGTCGGCGGAACAGCTCGATTCCCGGACCGCCAGCGCATTGGTGATGGAATCGGCGA  
ACTTGGCCACCCGCTGGGTGTTGACATCCTCGACGGTGGGCAATTGCGCCTCGGTAAGCTTTGCCGCGTAGCCTTTTC  
ATC

Clone Rv119

.....Rv119SP6.seq:.....

ATACTCAAGCTTCACTGACAAGGGACGAATTCGTCGGCCGCCTGTTGACTGGGTGGTGGCCGAGCTGGTCGCCACCA  
CTCAGGCCGCGGTACGGCGGTACCGGCGCGGGAGCAAACCTCGCGCGGGCATGGCCAACTTCTTGCGGACCATCACCG  
CAGACGCCCCTTCGGACCCCTGCTGTCCACCACACAGTTGGCCAACGCATTAATCACCCGCAAGCTTGCGGAATCCA  
CCGCCCTGTTTCG

.....Rv119T7.seq:.....

TCCATCACCCGATGTGGCNGGAGCACTGCCATGTCGATCTCAACTACCACCTCCGGCCGTGGCGGTTGCGCGCCCCGG  
GGGGTCCGCGCGAACTCGACGAGGCGGTTCGGAGAAATCGCCANCACCCGCTGAACCGCGACCACCCGCTGTGGGAGA  
TGTACTTCGTTGAGGGGCTTGCCAACCACCGGATCGCGGTGGTTGCCAAAATTACCATGCGTTGGCTGACGGTGTG  
CCTCGGCAAACATGATGGCACGGGGGATGGATCTGCCGCCGGGACCGGAGGTTCGGCCGCTATGTGCTGACCCCGCTC  
CTACCAAGCGGCA

Clone Rv11

.....Rv11SP6.seq:.....

AGCTTTGCAGTTGCTGAGTAATGTCGGCCAACGTACCCACAACCGCGATGAATTCAATCATGCCGCCAGGGCGGCCA  
ACCCAATGGTGGCCGCGAGCGGCAGCTCGATCGCAGCGCGGAGGTTGCCGGCCGCGCAGTTGATTACGAACAGGGTGA  
GGTCATAGGCGGGCAGGATAGTGACGAAGGCAAGACCTCCATCTGCCGTGCGAAGAAGTATCGAG

.....Rv11T7.seq:.....

AGCTTCAGAACAGGCCTGTTGTGGGCGCACCCGGCTCGCCGAGTTCTGCACGCACCGCCTCAAGTGCGGCCCCGCACCG  
CCGGCATCTCCCGGTACGCAGGGCCGCGGCCCGCGCCGAGCGACGGCGTGTTCGCGCAGTTTCGCCGTCAATGATGC  
TGACCTGATCGGCCACCCGGGCGTTCTCGGCGTCGTCGCGTTCACTAATCGCGGTGCTCAGCAGCGTCTCGACAGCCA  
CCACCCGAGTGCGGACACAGCTGCTCCACCACGGACCGCAGCGATGCCCCGTC

Clone Rv120

.....Rv120SP6.seq:.....

ATACTCAAGCTTCAGTTCCTCCACGACGCGTTCCCAAATGAATTTCCCGATCCCACAATCTCGGTTTCAGATACAGGTC  
GCCATACCCCTTACTTCGGCAACGCTGGGCGGATTGGCCCTGCCGCTGCACCAAACCATCAACGCCTTCAAATTGCCG  
GCAATCTCGTTTCAGCCAATCCAT

.....Rv120T7.seq:.....

GCTCTACGCCGCTACGGGTGGAACATGCATCCCGAGCAGATGCTCGAGCGCGCACCCCACTCGCCGATGGCCGGAAC  
CGGCTGTTACCCGGGTGGCGGCTGACGTTTCGGCGGCGAGGACATCNGCTGGGAAGGGGCGCTTGCCACCGTCGTCNA  
AGACCCAAATTCGAAGGTGTTTCGTGCTCTACGACATGACCCCGGCGGACGAGAAGAACCTTGACCGGTGGGAAGG  
CTCCGAGTTCGGTATCCACCAGAAGATCCGATGCCGCGTGGAGCGCATTTCTCGGACACCACAACGGGATCCCGTCC  
TCG

Clone Rv121

.....Rv121SP6.seq:.....

ATACTCAAGCTTGCCAAAGAGACCTCGTCCACCAAGCAGGACGCGACCGTCGAGGTGGCGATCCGGCTTGCGCTCGAC  
CCGCGTAAGGCAAACAGATGGTTTCGCGGCACGGTCAACCTGCCACACCCGGCACTGGTTAAGAACTGCCCGCGTCGC  
GGTTTTCGCGGTGGTGAAAAGGCCAATGCCTGCGTTTGCCGTGGGGGCGGATGTTGTCGGGAGTGACAATCTGATCA  
AAAGGATTCAGGGCGGTTGGCTGGAATTCATGCCGCAATCGCGACACCGG

.....Rv121T7.seq:.....

CCACGGCGTGGATCAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGATGTGCGCGTTAGCGC  
CGGATTCACCACATCCCTTGCGAAAGTCCGTTGGGTGCAATGATGTAGCGCTTCTCCCATCGAGATAGTGGAGCA  
ACGCAATCCGTGCGGTACGGTTTCGGGTTCGTAATGATGTGCGCGACCTTGGCGTTGACACCATCTTTGTCATTGCGGC  
GAAAGTCGATCATCCGTAAGCGCGCTTATGACCGCCGCTTTGTGCCGGGTGGTAATCCGGCCATGCGCGTTGCGTC  
CACCGCGACGTGCAGCGGGCGCACACGCGACTTCTCCGGGGTTGACCGGGTNATCTC

Clone Rv122

.....Rv122SP6D2.seq:.....

GCAGCATGACGGCGGTAGCGAACACCGCCGGATGCAGCGCAAGTAGCGTCGATGTGCTCACGGAATCGCCCCGGCACCC  
GCGATCTCGANGATCACCAGTGCCACCCCTGCAGCGCNACACCGACGATTCCGTACACCGCCACGCCGATCAGGCCCC  
TGGGCCATCTGATTGGAGCTGGCGTANATGGCGCGATGGTGACGATGGCCAGCGCCACATACATTGTGGCGGCCAGA  
ACCACGGCGTTGGGGCGGCGGTTCGATGAACACTAGGCGACGCAGATCGCCCCGGGTCAACAGGTTGACCATCAGAAAG  
CCTGCGACTAGCACGGCGGCCGCTAGGAAGTACAAGAANGTGGCCACCACCCCATGCAGGATCGGGGTAAGGCTGA  
TGGTCCCGAAATCGACTCCGGCCTAATACATGACTCTCTCTTTGCGTCATCGCCTTACTTGTGCGCGGAA

Clone Rv

.....Rv123SP6D2.seq:.....

GGGACACACCTCGATGCTGCCGCNATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGC  
TTCCGCCGCGGGCGTGACGCATCCCGTTGACCGGCCGGANCTCTCTA

.....Rv123T7D4.seq:.....

TGGGCGCCTCTTTTCGGCCTTCCNNTTTAAACGNAGCANGACATTTCTGGGTATCGAGTTGTACTGGATGGTGTGGCG  
ATGTCGGTGATCCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCGGGTTGAAAGAGGAAATTGGG  
GCCGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGAGTGGTGACGGCTGCCGGCATGGTGTTCGCC  
GTTACCATGTCGTTGTTTGTGTTTCAGCGATTTGCGAATTATTGGTCAGATCGGTACCACCATCGCCTTCCC

Clone Rv124

.....Rv124SP6D2.seq:.....

CCGATCGGCGCCGCANCTGGTTGGTGTTCGGATGAATCCGCAGCGAAAATGTAGCTGCGGTGGCGTGTGCTGACTCG  
TNGGCGTCGACGCTCGTGGCAGCCACCGANCGGTTGGTCCAGGATCTGGATGGGCAAAGTTGTGCGGCCCGGCCGGTG

ACGGCCGATGAGCTGACCGAGGTCGACAGCGCCGTGTTGGCTGACTTGGAACCGACATGGAGTCGCCCCGGTTGGCGT  
CACCTCAAGCATTTCAATGGTTATGCGACCAAGTTTTTGGGTTACGCCGTGAGACATCACGTCGGAGACTTGGATGAGC  
TGTGTCTGCCAGATAGCCCCGAATCGGGACGACCGTGGTCACGGTGCGTCTGACCACTCGGGTCGGGTCGCCCCGCGT  
ATCGGCATGGGTGCGTNATCACAGCGACACGCGCCTGCCAAGGANGTNCGGNCGGACC

::::::::::Rv124T7D4.seq::::::::::  
CGGGTTGCGGATCCACGCGTGC GGTTGTCAGCAGCTACGGCACTGAACCGCGCCACAGCTCGCCGATCCGCTTTCCG  
GTGGTTCTCGATCGACTCGCCGTAGGCGATGCGCAGCGCCTGCTCGAATATCGGGTACACGTAGGCCGGCCTTCCNC  
TTTA

Clone Rv126

::::::::::Rv126SP6.seq::::::::::  
CTTGATTTTGATCATCATGACGATCATCACCTAATTTTGTACCCGCACTGGTTATCGTGGGTACCGTCGTGCTTTC  
CATGGGCGCCTCTTTCCGGCTTTCCGTATTGGTCTGGCAGGACATTCTGGGTATCGATTTGTACTGGATGGTGTGGC  
GATGTCGGTGATCCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCCGGTTGAAAAGGAAATTGG  
GGCCGGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGGAGTGGTGACGGCTGCCGGCATGGTGT

::::::::::Rv126T7.seq::::::::::  
GGGGATCCCTAGATCGACCTGCAGGCATGCAAGCTTGGCGTGTGCTTCCAACCCGAATTGGCTTTCCGGCGCCATCGGT  
GAGGCGGGACACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGG  
AACGCTTCCGCCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCG  
GAGCNACTGTCAAGGCGCGTGCCAGGTGCGCCGGGCGCACGGTGCGGACAAGGTGGTGTGGCGGTCCCGATCGGCC  
CAGACGACATCGTGCGAGATTGNCGGGTACGCCGATGAGGTGGTGTGTTTGGCGACGCCGGCGTNGTTCTTCGCCG  
NCGGGCANGGTTACCGCAACTTCACCCAGACCTCCGACGACGAGGTGGTGGCGTCTCCTGGATCGTGCTC

Clone Rv127

::::::::::Rv127SP6.seq::::::::::  
AAGGCTGCAGGTGCAAGCGGNTGGTTACGACTCCCTGTGTGTGATGGACCACTTCTACTATCTGCGTCTACACGGCCC  
TTGGTGCGCTGGCCACGGCGACCGAGCGGCTGCAACTGGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCCCGACC  
CTGCTGGCAAAGATNATCACACGCTCGACGTGGTTAGCGCCGGTCGAGCGATCCTCGGCATTGGAGCCGGCGGGTTT  
GAACTGGAACACCGCCAGCTCGGCTTCGAGTCCGGCACTTCCAGTGACCGGTTCAACCGGCTCGA

::::::::::Rv127T7.seq::::::::::  
CTTTCCGGGTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCGGGCACCTACTACGTGCACTCCAACCTACTT  
CATCCTGACGCCGGAACAAATTGACGCNGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACTACAT  
CATTCGCACGGAGAACCTGCCGTGCTACAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGT  
TCAACCAAACCTTGAAGTGATTGTTAACCTGGGCTACGGCGACCCGGCCTATGGTTATTGACCTCGCCGNCCAATGT  
TGCGACTCCGTTCCGGTTGTTCCAGANGTCAGCCCGGTGCTCATCGCCGACGCTCTCGTCN

Clone Rv128

::::::::::Rv128SP6.seq::::::::::  
CGGTCATAGCCCTCGGGTCCGGCCAGCACTCCGCGAGGCTTCGTGCGGGTGGTTCGCGACGCGCATGGGCCACCATCGCA  
TTCACCAGGTCTGCGCGAATCACAGCACGTAGACGGTTCTTTTCTAAGCAACACCGAAGTTTACGACCCGAATGC  
TCCGGGAAACATGTACGGTAGGTGCGTATTCGGGCTACCGGCTGAGCATTGAGCACGCCGGCCAGCACCGCACGAGC  
CAGGCAATCAGCCGCGCGCCGACCGATCGCGGTGACCAGCTGAGTCTCCGGAGACAATGCGGCCGGCACGCCGNCTC  
CGGCGGCACCGCTACNGCGCCCCGTGG

::::::::::Rv128T7.seq::::::::::  
GTGATGGCACGCCACCGCGACACCACCGGCTGCGCTACNTCGAGCCATACCGGGCGGAGCTACATCGGGCTCGGCCGCG  
CCAGTGTTCGGGCCCTCTTTGAGGTGAGGTGATACCGATTGCGCATCCGCANCCGNCNCCCTGGACGACAGAACC  
GTGCCCTACGAGTGCTTGTGCGGGCGGGGCCAAAGAACAGCTTGGCATCTGGCGGATTGGCCGGCGCGCGCTGGTC  
GCCAAGGACGACGCCGTTCCGGTGCTGATCGACGACGCGCTGGGGTTACCGATCCGGAGCGACTATCAAGATGGGGG  
AGGTCTCTGACACCATCGGCCCNACGGACATGTGATCGTGCCGACGTGCACTCCACCCCG

Clone Rv129

::::::::::Rv129SP6.seq::::::::::  
GCGAAAGTCCGTTGGGTGCAATGATGTAGCGCTTCTCCCCATCGAGATAGTGGAGCAACGCAATCCGTGCGGTACGGT  
TCGGGTCGTACTCGATGTGCGCGACCTTGGCGTTGACACCATCTTGTGATTGCGGCGAAAGTCGATCATCCGGTNNG

CGCGCTTATGACCGCCGCTTTGTGCCGGGTGGTAATCCGGCCATGCGCGTTGCGTCCACCGCGACCGTGACGCGGGC  
GCACCAGCGACTTCTCCGGGGTTGACCGGGTGATCTCGGCGAAATCAGATACGCTGGCGCCGCGACGACCAGGCGTCG  
TGGGCTTGTNCTTGCGAATTGNCATGTCTAATCANGTCTTTCTCTCACGCTCTCGTCGCCGGGCTAGGCCGCATTGCC  
CTGCTCCTCCTCATCGCTTCGCTCTGCATCGTCCCCGGGCTAAGCCCGTGCCCCGAAA

::::::::::Rv129T7.seq::::::::::

GATGGTTCGCGGCACGGTCAACCTGCCACACGGCACTGGTAAGACTGCCCGCGTCGCGGTATTGCGGGTTGGTGAAAA  
GGCCGATGCTGCCGTTGCCGCGGGGGCGGATGTTGTGCGGAGTGACGATCTGATCGAGAGGATTTCAGGGCGGCTGGCT  
GGAATTGCGATGCCGCGATCGCGAACACCGGATCAGAATGGCCAAAGTCGGTCGCATCGCTCGGGTGCTGGGTCCGCGC  
GGCCTGATGCCCAACCCGAAACCGGCACCGTCACCGCCGACTCCCCATGGCGTCCCGGATATCAAGGGCCGGCAAAT  
CAACTTCCCGGTTGATCAGCAAGGCAACCTGCCTCCNCCTCCGG

Clone Rv130

::::::::::Rv130SP6.seq::::::::::

ATACTCAAGCTTCGTATAAGACCATGGTGCGCTTTCTTTACCCCGTCCAGAGTCGGGGGCATCCGCACCGGCTCGCA  
TCGCATCATCTCCCACGACGGGCGGCTCATCAGCTTGGGCCATTTCAATGTACTTGATACCCCGCGCTGCGGGTAGG  
CCACTGCGACAATTCAAACACGGTGTCACACGGTGAATAGTGTGAGATGGGCTCTGATCAACCGTCGCAAACCCGCT  
TTCGCATCAATAGCGGAATCCACCGGGTTGCATGGAGGCTGCTGACCTTGGAACAAATTTTTTCATTACAACAA  
AACAACCGCCNCGGAACTTTGCA

::::::::::Rv130T7.seq::::::::::

CGAATTCGGCGTGACCGCTATGGGTTCAGCAGCGGCTGGCGCCGCACACCCCACTGGCCCGGGTGTTTTCGCCCCG  
AACCCGGATCATGGTGAGCGAAAAGGAGATTGCGCTGTTGATGCTGGGATTCGCCACCGCGAGGCCATCGACCGATT  
ACTCGCCACCGGGGTGCGAGAGGTGCCGCGAGTCCCGCTCCGTGACGCTCTCCGACGATCCATCCGGCTTCCGCGCTCG  
GGTGGCGGTAGCCGTGATGAAATCGCTGCCGGCCGCTACCTGCAAGGTGATTCTGTCCCGTTGTGTCGAAAGTGCCCTT  
TCGCGATCGACTTTCCGTTGACCTACCGGCTGGGGCGCTCGGCACAACACCCCGGTGAGGTCGTTTTGTTGCAAGTTGG  
GCGGAATCCGTGCTCTGGGTTACAGCCCCGAACTCGTCACGGCGGTGCGCGCCGACGGAGTTGTTATACCGATCCGT  
TGGCCGTACCGCGCTTGGGC

Clone Rv132

::::::::::Rv132SP6.seq::::::::::

TCAGACTCCACCCAGCCAGCAGGCAGCGAAGCTGAATCCTCCAACCGGGTTGTCGATCCGGACAGGTTGGGGTGCG  
TTTGGGGCAATGACAGGTGGCGGCGGTGCGTTCGGGTGCGCCGGCGGAGGTGCTGCGTTGGGATCGCCCGGCTGGGCA  
TTCNCGCTGTTGGCGGCGGCGGTGTTGGGGGGGCAACAGGTGTGCGCGGTGCGGGTGGCGCTGCAGCGGTGACGGC  
GGCGAAGCGGCCGTTGTGGGTACCGGGGGCGCTGGCTCCGGATCGGCGTTGGCGGTGCGGGGCACCGCAACGGTCACC  
AAGCTGGCGCTGGCCATCGCCGCGATAGCCAGTGCCGCCAATCGTCCCTTGCGACGTGTCAAGTNGGGGTCCACCTGA  
TGCATGGCCAAAGAACCTACCGTGTTAACGGCNCAACNCAAGGACCGCGCCGGTCCGN

::::::::::Rv132T7.seq::::::::::

TTTCGCGGTACCCGCTCAACTTTGTGTCNACCCTCAACGCCATTGCCGGCACCTACTACGTNCACTCCAACCTACTTC  
ATCCTGACGCCGGAACAAATTGACGCGAGCGGTCGCTGAACAATTGCGTCCGTCCACGAAAGAACCTTTTNCNT  
CTTTCNCACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGTG  
TTTCAACCAACACTTAGAGTGTAATTGTAAACCTGGGCTAGGGGAAACCGGCTCTAGTTTTTCCACCNTCTCCGCCCC  
NTGTTTCGAATACTCCGTTCCGGTTGTCCCCAAA

Clone Rv134

::::::::::Rv134SP6.seq::::::::::

GCTTCCGGCTCGTATGTTGTGTGGAATTGTGACCGGATACCAATTTACACAGGAAACAGCTATGACCATGATTACGC  
CAAGCTAGTTAGGTGACACTATACTCAAGCTTGCCGGCTGGTGGGCCGACCACTTCGATGGCAGCAGCCGTGA  
ACTGCTGCCCGGCAATTCTTGGTTCGGCCGACCGTGGACCGCGGCTGGGATTCAGAAGGTGCCCGATCCCGC  
CCCTGGGAAAACCGCGTGACCTTACTTACAGACCAACGAC

::::::::::Rv134T7.seq::::::::::

CCGATCGACTGATGCGCCGACAACCACGCCCAACAACCTGGAATGAACCGTCGTGACCATCATCAGCACGCGGTTGTA  
GGCGACTTGCGACATGTTCAACCCGCCGTACTCGGACGGAATCTTCAAACCGAAACAGCCAGCTCGGCCAGGCGCTTT  
CACGTACTCGTCGGGGATCTGGGCACCACGCTCGAGGACGCTGCCGTCCACGGTGTCTAGGAATTCGCCGAGTTTAC  
CAGAAACGCTCGGTCGGGCTCCTCGGCGTCCGACGGCTTGGGAAATGGGTGTATGAGCCCTACGGGAAACCGGCC  
CACAAAGAGTTCTTTGGCGAAGGACGGTTATCCCAACCACTTTCGCGAGATTCTCGGCAAGGGCCCGCGCTTGCTC  
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## Clone Rv135

:::Rv135SP6.seq:::

TGCATCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG  
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AGCGCAGCGCTTCCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCGGCGGTGCGGTGACGGTGCTCGGGCAGCTCGG  
CCGCGACAGCCGCTGACCCTGAAACCAGCTTCCATATCCCGCGACGAACGACGCCAGTCCGCTACGTAACCCCTCCG  
CGACTGTCCATGGACAACAGCGCGTTCTCCACCAGCCGGGCCCGGGTGTGGGTGTTTCGGCGACCGGCAGCCAGGTG  
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:::Rv135T7.seq:::

GGGGGCGCTGCTGGTATAGTCGCTGACCGGTGACGGTTTCGACAATGTGGTGCCGGTTCGGCGGCTACGTGCCATCGA  
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CGTCGTCAATGGTCGACACCACGACGGAAGACGCAGATCGCGTCAAGCATGTGTGCCGCGGATTATCAGGACTGAC  
CTCCTGGCTGACCGGCATGTTTGGTCGCGATGCCTGGCGCCCGGCCGGCTGGTCTGGTGGCTCGGCTCGGATAGCGAGGT  
CAGCGAATTCTCGTGGCAGCTCGAAAGGGTCTGCCGGTGCCGGTCTTTGCGCAAACGATGGCGCAGGTTACGGTTCG  
GCGGGGTGCGGCTGGCGCGGCCAGAGCACGAGTTCACCGATGCGCAGCTAGTGGCGACAGCGTCAGCCAAAC

## Clone Rv136

:::Rv136SP6.seq:::

TGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG  
CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCCGTACAGGTGCGCTCCAACACGGCGGGGAAGCGACACCA  
GCCTACCGAGCTTGGAGTCCAGGACGCCAGCGGCGGCGTGGTCTGCGTCTGGTGCCGCGGGGTGGCGTTGGCTGG  
CAACGATCTCCACCCAGCCGCTCGGGTTACCCACGATCTCGGCATAGACCGGGCCGAGGCCGGTGGCATAACCGTATT  
GCGTCAATTGGGACGCGGTTGTGCATTGCGCTAGCTCGGTTGCCACACCCGTAGGGGTTTCAGCTTGGCGGGTTCGG  
CGGGCCCCAGCACCGCTGTCAACATGCCCGCCAAGCCGACCTGCGGCGCCACCAACT

:::Rv136T7.seq:::

CGGCATGACCACCGACAGGCCGACTGGTCTGTAACCTCGAACGCCGGGGTGTGATGTCCAGCCGCTGAAGTCGTC  
CTGCGCGCGCAGGCCGTCGAGCAGGTACAGGGCGGGCGAGTTGGCACCACCACTTTGGAATTGGACCTTGATGTCAGC  
GCCCATCGACGGCGACGGCAGCTGACGGTACTCCACCGGCAAGCCCGGCCGGGAAAATGCCCCGCGGTGCGCGTGCC  
ACCGACGGCGCCGACCAGACCCGACACTAGGGCCGCGCCGACGGCCCCGACCACGAGTCGACGCGACATACCCGTGAC  
GGCGCCACGAACCTGTCAACAAGCTGCATTCTTGCTTCCCTCATCTCATCTCAACGCATCCATGCATGTTTGGGCG  
CATCTGAATTANGTCAGACTGCAGGCGCTGGGCGGGCAGTGCTCGTGTATCAACCACAACCTTCGGGCGT

## Clone Rv137

:::Rv137SP6.seq:::

TTCCAACCCTAATTGGCTTTTCGGCCCCATCCGTGAGGACGGGGTGCGGGTGCTCAACAACAACGTCGTCGCGGGGACA  
CACCCTATGCTGCGCCATGGACGCGGTCCAACGCAAGCAGCTGATCGAGCTACAACCCCGCGCGGAACGCTTCCGC  
CGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCGGAGCGACGGCC  
AAGGCGGCGTGCCACGTCGCCCCGGGCGCACGGTGCGGACAAGGTGGTGCTGGCGGTCCCGATCGGCCCAAACGACATC  
GTGGCGAGATTGCGCGGTACGCCGATGAGGTGGTGTCTGGCGACGCCGGCGTTGTTCTTCGCCCTCGGGCAGGGT  
TACCGCAACTTCAC

:::Rv137T7.seq:::

CAGGCATGCAAGCTTTCCGCCGATACCCGCCATGTCGCGCACATCCAGGACTTCTGGGGGATCCGCTGACAGCGGCG  
GGATCCCAAAGTGCGGATGATCGGGCCGCTACGTCGTGGTGATCTCGTCGGTAACAACGAAACCGAAGCGTATGAC  
TCGGTCCACGCGGTGCGGCACATGGTGGACACCACACCGCCACCGCACGGGGTGAAGGCCTATGTACCGGTCCGGCA  
GCACTCAATGCCGACCAGGCCGAGGCCGGAGACAAAAGTATCGCTAAGGTACCGCCGATCACNAGCATGGTGATCGC  
AGCAATGTTGCTAGTGATCTATCGTCCGTAATTACCGCGGTTCTCGTCTTGATCATGGTCGGCATCGACTCGGCCAA  
TCCGCGGATTATCGCCTTGCTCGCCGAACACAACATTTTCACCTTTCACATTTGCACCAACCTGCTCTTCTCAT

## Clone Rv138

:::Rv138SP6.seq:::

CACTACTCAAGCTCTCTCNTCATTACCACCCCTGTAATTTGGGATGGGCAAAAAGGCGAAGCACCGCTTGGCCACNAA  
CGCCGGGAGGGACAATCTCGGGCGGCTATGGCTTCTCCCGGGAAGGCCCAACGTACGGCGTTTCAACACGTCGCGTC  
GCCCTCCGACCGCGAATCTCGGGGATTGGCACCACCTGNTACCACCCCTGGCCGGGCGATGATCTGCAGCGTCGCCG  
CGGGTAGTCCCCCGCCGGGCGGCTACAGTCTGAAACCCCGATGACCATCGATGTGTGGATGCAGCATCCGACGCAACG  
GTTCTACACGGCGGATATGTTCTCTCGCTGCGCCGGTGGACCGGTGGGTCTATCCCCTGAAACCGACATCCCN



## Clone Rv142

:::Rv142IS1081.seq:::

GAAAGTGCCCCAAGGTGTTGGTGAAACTCGCTGGACGGTCCCCAGGATGTTGGCAGCACATTCACCGGACATGACCGG  
AGCAAGACCGGACATCCTCCCATAACCGTCGTCGCCGTGTACATCCGTAGCCCGTCCTGGCAGGTGCTGGGTTGAACAA  
AATCAGCCCAACACCTGCCACGACGAAGAAGCGGGTTCGCGCTGGCATGTCTTGTGGCTCGGCGATCGAATTCTACGA  
ATTCCTTATCTACGGGACCGTGCGGCGCTGCTGTTTCCACCGTGTCTTCCACACCTGGATCCCACGGTGGCCGC  
CGTGGCCTCCAAGGGGACATTTGCTGTGGCGTTCTATCCCAGCGCTTCGGCGCGGCCGTCTTTGGATACTTTGGAGA  
CCGCCTCGGCCGCCAGAAGACCTGGTCGCCACACTGTTGATCATGGGCCTGGCAACCGTGACTGTTGGGCTGGTTCC  
ACGACAGTGGCCATCGCGC

:::Rv142SP6.seq:::

ATATTCAAGCTTTGTACACCAAGTGTTCGACCAANCGCTCCATCCGGCGAGTGGATACTCCAGCAGGTAGCAGGT  
CGCCACCACGCTGGTCAGTGCAGCTTCATCTCGCTTGCAGCGCTGCAGCAGCCAGTCCGGGAAATAGCTGCCCTGGCG  
CAGCTTGGGGATCGCGACGTCGATGGTTGCGGCACGGGTGTGAAATCACGGTGGCGGTAGCCGTTGCGCTGATTGGA  
CCGCTCATCGTGCCTTCGCGGTAGCCNCCCCGCACAGGGCGTGGCTTCAGCCCCATCCAAGGCGGCGATGAACG  
TCGAGAGCAGCCGCGCAGCAAATCCGGGCTCGCTGTGCGAGTTGGTCAGCCAGAAGCTGCTCGGTGTCATAAGATG  
AGAAGAGGTCACTGCGTCTTTCTTCG

:::Rv142T7.seq:::

CAGGCATGCAAGCTTTTGTAGCGTCTCGCGGGGCGAGCTTCGCCGGCAATTCTACTAGCGAGAAGTCTGGCCCGATACG  
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CCGCTTGGCGACGGCGACGCGGTAGGTGGTCAAGTCCGGTCTACGCTTGGGCCTTTGCGGACGGTCCCGACGCTGGTC  
GCGGTTGCGCCGCCAAAGCGCGGGTTCGGGTGCCATCATGAATGCCTCACCGCCGCCGCACTGCACGGCCAGTGCCCC  
GGCGATGTCAGCCATCGGGACATCATGCTCGCGTTCATACTCCTCGACCACTCCGCGGAACAGCTCCATTCCCGGACC  
GCCAACGC

## Clone Rv143

:::Rv143SP6.seq:::

ATACTCAAGCTTTTGGCTGGGTGCGCTTCCAATTACAGCGTGACCCGCTATGGGTGTCAGCAGCGGCTGGCNCCGCACA  
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TTCGCCACCGCGAGGCCATCGACCGATTACTCGCCACCGGGGTGCGAGAGGTGCCGAGTCCCGCTCCGTCGACGTCT  
CCGACGATCCATCCGGCTTCGCGCGTTCGGGTGGCGGTAGCCGTCGATGAAATCGTGGCGCCGCTACCACAAGGTGA  
TTCTGTCCCGTTGTGTCCAAGTGCTTTTCGCGATCGACTTTCGCTTGACCTACCGGCTGGGGCGTGGGCACAACACCC  
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GCCGAC

:::Rv143T7.seq:::

CAGGCATGCAAGCTTCAACCTATTGACGCATTGTGCGAACTGACGGCGCCCGCGCATGGCCAATCCGGAAGACCATCA  
TTGGCCAGTGGCCGGGCGCTAACAGGTTCCAGCCCCCACCAGTGCCGCTCGAACATGCGGTGCAACCCATTGCGAGG  
CCGGCAGGGAAAGCACCGCGGAAGCCGCAAAGGGCTGCAGTTCCGCGCCCAATAGTGTGCTCCGCAACCAAGATGCGCT  
CGAAAACCGCCCGCCGGCAGTCAGCGCACCCGACGCGAGGTGAGAGACGTCGTACGCGCGCCACATGGGGTGCCAAT  
CGGCACGGCAGGTAGGCCGCGCGCAACCCCAACGCGTGGTGCATGCCACGGTCCGAGGAGGCCACCACC

## Clone Rv144

:::Rv144SP6.seq:::

ATACTCAAGCTTCCCGGCCGCGAGGTGACGGCGCGGCTAGCGCCACTTGATGCCGCACCCGATCGACGGNCGTTGGTC  
GGGGTTGACTGGCCGCCCGGCGAGCAGGGCGTCAACCGCGGCGCCGACGTGCGCGGCCGTACCCGGTCGGCCATTGCC  
CGGGCGGGAGTGTGTCGAGCTGACCACGGTAGACAAGTCCGGCGTGGCCGTGGAAGACAAACGTGTGCGGTGTGAGGC  
CGCGGAGAAGGCGCNGGCGACGTCTCGGGTTTCGTGTCGATAGAGATACGGGAACGTCCAGCCGTGGCGGCGGGCTCGGC  
GACCATCTGATCGGGCCGTCCTGCGGGTAGGTGACCACTGCTTACTGGAGATACCGACCATCGGGACCCCTTGATC  
GGCAGGTCCTCGGCCGACCGTGGCCAATCCGGCGGCGACGTGTGCGCCGTACCGGCCAGTGGTTT

:::Rv144T7.seq:::

CAGGCATGCAAGCTTTTANCANCATCAACCCGCCCCGCACACGACCGGACACGATGTGATGCCATCGAGGTGAATGT  
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GACGGGCCGCTCTCACCGCAGGTGACCTCGATCACCGAGACAGCCGGCCGTTATACTACGCAACCCCTACCGTGTCA  
CGCCCAAACGGCGCTGGTGGTCGATTGCCGGAGTGACACCCCGCACCCAGTGTGTCGCCGGATCCGCCGACCAATCC  
CGCACCCAGTGCAGCAACCCGAAATCACCGTGATGCCGTGTAACGACACCGACAGTAACGTCACTACGGCCGCC  
ACGCCGACGCCGAACACACGACATGATGATCGGCTG

## Clone Rv145

:::Rv145SP6.seq:::

ATATTCAACCTTGACACATTGACGATACCTTGGTCACGAGACCCAAAAGCTGGCCTCCACCGCGCGCCGGGGACCA  
CGGTCATACCTTGANNNGCTTTTCGATCGTTGATGCTGCGTCTTGGTCCGCGGAAACCGCAGGCTGGCATATGCACGT  
GGGCGCACTGGCGATCTGCGATCCCCACCGATTGCGCCGAATACAGCTTTCAGCGGCTCCCCAAGTTGATCATCGACC  
GGTGCCGGATATCCCGCACTTGCGGTGGCGGGTCACCGCGCCCCGCTCGGACTGGACCGCGCGTGGTTCGTGAGG  
ACCACGAAC

:::Rv145T7.seq:::

CAGGCATGCAAGCTTCATGCGCGGCATGATAGCCACATGCACGCAATCGAACTCAGCGAAACCGCGGGCCAGGCG  
TCTTACGCCACCTCACCAGCGCGAACCTCAACCGGCCACGGAGACCTCCTGATC

## Clone Rv146

:::Rv146SP6.seq:::

ATACTCAAGCTTGATTTTGATCATCATGATCATCACCCGAATTGTGGTAGCCGCAGTGTTATCGTGGGTACCGT  
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GGTGTGGCGATGTCGGTGATCCTGCTCNTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCCGGTTGAAAGA  
GGAAATTGGGGCCGGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGGAGTGGTGACGGCTGCCGGCAT  
GGTGTTCGCCGTTACCATGTGCTTGTGTTGTGTTTCAGCGATTGCGAATTATTGGTCAGATCGGTACCAACCATCGGCCT  
GGGCTTGCTGTTCGACACCCCTCGTCTGCTCGTTCATGAAACCGTCCATTGCTGCCCTGCTGGGACCTGGTTCTGGT  
GGCGCTACGGGTGCGCCCGCGCCCGGCAGTCAAATCTTCCGCCG

:::Rv146T7.seq:::

CAGGCATGCAAGCTTGCGGTGCCGTTCCAACCCGAATTGGCTTTCCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTC  
AACGACGACGTCGTCCGCGGGACACACCTCGATGCTGCCGCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTA  
CAACGCCGCGCGGAACGCTTCCGCCCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGAC  
GGCATCGCCACCGGAGCGACGGCCAAGGCGGCGTGCCAGGTGCGCCGGGCGCACGGTGCGGACAACGTGGTGCTGGCG  
GTCCCCATCGGCCAGACGACATCGTGCGGAGA

## Clone Rv147

:::Rv147SP6.seq:::

ATACTCAAGCTTTACGGTGATCGCGCATCACCTGGTTCATGAACTGGAAGCAGCGCAGCGCTTCTTTTCGGCCGCA  
ACATGAGCCAGCTCTCGTCGGCGGTGCGGTGTCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCTGAAAC  
CAGCTTCCATATCCCGCGACGAACGACGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCGTT  
CTCCACCGACCGGGCCCGGGTGTGGGGTGTTCGGCGACCGGCAGCCANGTGGTCCACACTGCCGAAG

:::Rv147T7.seq:::

TAGTCGCTGACCGGTGTCAGGTTTCGACNATGTGGTGCCGTTTCGGCGGCTACGTGCCATCGAGACACTGGCGCAGGCT  
ATCGCACCCGTTATCGGCTACGAGCAAATCGCGGTATGCGTTCTTGAGCATGAGTCGGCGACCGTCGTGATGGTCGAC  
ACCCACGACGGAAAGACGAGATCGCCGTCTANCNTGTGTGCCGCGGATTATCAGGACTGACCTCCTGGCTGACCGGC  
ATGTTTGGTGCGATGCTTGCGCCCCGGCCGGCGTGGTTCGTGGTTCGGCTCGG

## Clone Rv148

:::Rv148SP6.seq:::

ATACTCAAGCTTTCCGCCGATACCCGCCATGTCGCGCACATCCAGAACTTCTGGGGGGATCCGCTGACAGCGGCGGGA  
TCCCAAAGTGCGGATGATCGGGCCGCTACGTGCTGGTGACCTCGTCGGTAACAACGAAACCGAAGCGTATGACTCG  
GTCCACGCGGTGCGGCACATGGTGGACACCACACCGCCACCGCACGGGTGAAGGCCTATGTACCCGTCGGCGAGCA  
CTCAATTGCCGACCAGGCCGAGGCCGGAGACAAAAGTATCGCTAAGGTACCGCGATCACGAGCATGGTGATCGCAGCA  
ATGTTGCTAGTGATCTATCGCCCCGTAATTACCGCGGTTCTCGTCTTGATCATGGTCGGCATCGACCTCGGCGCAATC  
CGCGGATTCTGCTGCTCGCCGACCACAACATTTTCAGCCTTTCAACATTTGCGACAACCTGCTCGTTCATG  
CGATTGCNGCGAAC

:::Rv148T7.seq:::

CAGGCATGCAAGCTTGCGGTGCCGTTCCAACCCGAATTGGCTTTCCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTC  
AACGACGACGTCGTCCGCTGGACACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTA  
CAACGCCGCGCGGAACGCTTCCGCCCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGAC  
GGCATCGCCACCGGAGCGACGGCCAAGGCGGCGTGCCAGGTGCGCCGGGCGCACGGTGCGGACAAGGTGGTGCTGGCG  
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TTGTT



## Clone Rv152

.....Rv152SP6.seq:.....  
CGCGGCGGCGCATTACCCCCGCTACCGTCAGCAGCTTGACGGCGGTAGCGAACACCGCCGGATGCAGCGCAGGTGCGT  
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.....Rv152T7.seq:.....  
GGGATCGAGGAACAGCGCGTTGAACTGATAGGTGCGGCCCGGCTCGAGCAGGCCGGCCATTTGTTTCGATGCGGTTACC  
GAAGATCTCTTCGGTGACCTGCCCGCCCGGCCAGCTCGGCCAGTGCCCGGCGTTGGCCGCCGCGGCGACGATCTT  
GGCGTCCACGGTGGTCGGGGTCATGCCCGCAGCAGGATCGGCCAGCGGCCGGTCAGCCGGGTGAACCTTCGTCGAGAG  
CTTGACCCTGCCGTGCGGGAGGCGAACACGGTCGGTGCGTATCTCGACCAGGCCCGGGCAACCTCGGGGGTGGCGCC  
GACGGTGAACAGGTTGCGCTGGCCACCGCGGGTAGCCGCCGCGCACTATGCCGATGCCAGGCCGCGGATCACCAGGTGC  
GGTCAGTCGGGTCAGGATGTCGCCCGGCCCGAGGTGGAAGATCCAGCGGGCGCCGGCCGCGTGGACACNGGTGATCTC  
GTCCACCATCGACTTTCTGATCA

## Clone Rv153

.....Rv153SP6.seq:.....  
TAACTCAAGGCTTGCGTTGAGGCCCCAGGCCCATCGACGGTTTGGCGGCCTTAAATGCACTGAGGTTCGTCATTGACC  
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GGTATATGACCTCGGTTTCTCGGGTGCTACCGCGTGCTTGTTCGAGGATGAACCTCGGCGTTGGAATTGTCCAGCCGGC  
CCAATTCATCGAGCGCAGATTCTGTACACATGGCCGGCGGCGACATACGCTTCACCGTGGATCTGCTCCACACGGACCG  
CCCTGTTCGGGATCCTGCTCACGGGTAAAGGAACTTACNTGGCNCTCGGTGCC

.....Rv153T7.seq:.....  
CCTTCTGCGCCACCCACACCGTCAACGCCCGGAAGTCGACGTCGTCCAGGCCATCGGCGGCCCTCACGGATGGATTTCG  
GCGCGGACGTGGTGATCGACGCCGTCGGCCGACCGGAAACCTACCAGCAGGCCTTCTACGCCCGCGATCTCGCCGGAA  
CCGTTGTGCTGGTGGGTGTGCCGACGCCCACATGCGCCTGGACATGCCGCTGGTCGACTTCTTCTCACGGCGGTG  
CGCTGAAGTCGTCTGGTACGGCGATTGCTTCCCCGAAAGCGCACTTCCCCACGCTGATCGACCTTGACCTGCATGGCC  
GGCTGCCGCTGCAGCGGTTCTGTTCCGAACGCATCGGGCTCGAAGACGTCGAGGAGGCGTTCCACAAGATGCATGGCG  
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## Clone Rv154

.....Rv154SP6.seq:.....  
ATACTCAAGCTTTGATTTTGATCATCATGATCATCACCCGAAGTGTGGTAGCCGAGTGGTTATCGTGGGTACCGT  
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GGTGTGGCGATGTCGGTGATCCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCCGGTTGAAAAA  
AGAAATTGGGGCCGGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGAGTGGTTACCGCTGCCGGCAT  
GGTGTTCGCCGTTACCA

.....Rv154T7.seq:.....  
ATTGNCTTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTCAACGACGACGTCGTCCGCGGGACACACCTCGATGC  
TGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGCTTCCGCCCGGGCGTGA  
CCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCGGAGCGACGGCCAAGGCGGCGTG  
CCAGGTCGCCCCGGGCGCACGGTGCGGACAAGGTGGTGCTGGCGGTCCCGATCGGCCAGACGACATCGTGCGGAGATT  
CGCCGGGTACGCCGATGAGGTGGTGTGTTTGCCGACGCCCGGCGTTGTTCTTCGCCGTCGGGCAGGTTACCGCAACTT  
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## Clone Rv155

.....Rv155SP6.seq:.....  
ATACTCAAGCTTTTCCCGTCCGTCTCGCCCAAGCGCGTGAGGCCGAAGCGGCTGGTTACGACTCCCTGTTTGTGATG  
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GCCACGGCGACCGAGCGGCTGCAACTGGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCCGACCTGCTGGCAAAG  
ATCATCACCACGCTCGACGTGGTTAGCGCCGGTCGAGCGATCCTCGGCATTGGAGCCGGTTGGTTTGAAGTGAACAC  
CGCCAGCTCGGCTTCGAGTTCGGCACTTTCAGTGACCGGTTCAACCGGCTCGAANAGGCGCTACAGATCCTCGAGCCA  
ATGGTCAAGGGTGAGCGCCAACGTTTTTCGGCGATTGGTACCCACCGA

.....Rv155T7.seq:.....  
CGGCCACCGGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCGCCGACTTTC  
CGCGGTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTTTCATCC  
TGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACTACATCATTC

GCACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGTTCAAC  
CAAACCTGAAGGTGATTGTAACTGGGCTACGGCGACCCGGCCTATGGTTATTGACCTCGCCGCCCAATGTTGCGA  
CTCCGTTCCGGTTGTTCCAGAGGTCAGCCCGGTGCTCATCGCCGACGCTCTCGTCGCCGGGACCAGCAGGGAATCGG  
CGATTCGCGCTACA

## Clone Rv156

:::Rv156SP6.seq:::

ATACTCAAGCTTGGGGTGGCGCTGTCGGTGGTGTGCTTGGCGGCGTGGTATCAACACCGCCACGAAATGGGGCAC  
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AACCCTGGCCATCACNTCCGGGTGTCCACACCGGAGGACCCGGCGTGGCGCGGTTTCGGCGAAACGTTGTGGGAGTTC  
CTGCCCCGAGTGTATCGGCGGCTTGGCGCTCGGCCGTTCAATTTGGAGGCCAACGGCTGCGTCGGCTCGGCGTCAGC  
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:::Rv156T7.seq:::

TCGCCACCGCACCGCGGCGAACGCTCAAAGGCACCTACTGGCAGCAAGGCCCCACACGTCACCCTGTGACCTCCTGCG  
CCGACCCCGCCGAGGTCTTGGCCGTTACCACCGAACGGGCGAGCCGGGAGTCTGGTACGCATCGAACAAAGAGCAAG  
GTGCATGGGCGGAGTTGTTCCGCCACTTCGTCGATGACGGGGTCGATCCATTGAGGTCCGTCGCCGCGTGGTTCGAG  
TGGCGGTCACTCCAGGTACTCGACCTCACAGACGAGAGGACTCGATCCCATCTAGGTGTGGACGAAACAGATCTTC  
TGTCGACGACTACACCACCAACCCAGGCCATCGCCGCCGCCGCGATGCCAACTTCGACGCCGTACTGGCCCCGGCGG  
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## Clone Rv157

:::Rv157SP6.seq:::

ATGAAATAAGAAGAGCACATCCCTCAGTCGGTTATCATCACTAGCGCTCGCCGCACCCGTGTAACCGATCATAGCGAG  
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GGAACAACTCCAGGTAGAGGTACACACGCGGATAGCCAATTGAGAGTAATAAACTGTGACACTCACACCTCATCAAT  
GATGACGAACTACACCCCGATATCCGGTCACATGACGAAGGGAAGAGAAGGATATCATCTGTGACAACTGCCCTCA  
AATTTGGCTTCCTTAA

## Clone Rv159

:::Rv159SP6.seq:::

ATACTCAAGCTTGTGCAACTCCTTCTTGAATACCGGCCGGCCATCCACAGATGCCCGGAAGAACTTCCAGGTACCCAT  
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GACGGTACCGGAGGGCAGCGACAAAACACTTATGCACTTGGGCGACCCGCCGAGACGGTGCACACCCATCCCGACGG  
CACAAGCTCAGCCGCGGCCGCTCTTGTCTTCTGTCGGATCGACATTCACCCACTTCTGACCGGGCTTGGCGGAAGGAA  
GCAGAA

:::Rv159T7.seq:::

GGTATAGTCGCTGACCGGTGACGGTTTCGACAATGTGGTGCCGGTTTCGGCGGCTACGTGCCATCGAGACACTGGCGCA  
GGCTATCGCACCCGTTATCGGCTACGAGCAAATCGCGGTATGCGTTCTTGAGCATGAGTCGGCGACCGTCGTCATGGT  
CGACACCCACGACGGAAGACGACAGATCGCCGTCAAGCATGTGTGCCGCGGATTATCAGGACTGACCTCCTGGCTGAC  
CGGCATGTTTGGTCGCGATGCCTGGCGCCCGGCCGGCGTGGTCTGGTTCGGCTCGGATAGCGAGGTGAGCGAATCTC  
GTGGCAGCTCGAAAGGGTCTTGGCGGTGCCGGTCTTTGCGCAAACGATGGCGCAGGTTACGGTCGCGCGGGGTGCGGC  
CCTGGCGGCGGCCCA

## Clone Rv15

:::Rv15SP6D2.seq:::

GACACTATATNATACTCAAGCTTCAGGTCAATGTGCGCCAAGCCCTGACGCTGGCCGACCAGGCCACCGCCGCCGGAN  
CCCTNTCTAGA

:::Rv15T7.seq:::

CTGTAGCCACCTGTTGCCATCCCGTCATGCCGACTCTGGTCATCTCGGATCCGCTGACACCCCGCTAAGGCTGCTC  
CTCTCGGTGCATTACCTACCGACGGCGAACNCCCCAGCTTTACGACTATCCGGATGACGGCACCTGGTTGCCGGCT  
AACTTCACCGTCAGCTTGGACGGCGGCGTACCGTCGATGGCGCCAGCGGGGCGATGGCCGGGCGCGGACCGATTCT  
GTCNTCANCTGTGCGGTGAACCTGCCGACGTCATCGTGGTGGTGTGGGCACCGTCGCGATTGAGGGCTACTCCGGC  
GTCGGATGGGTGTCGTCAGCGCCCGCACCGGCAGGCCCA



CCAATACGGTCGGTCCCACGATGACCCAGTACTACATCATTCGCACGGAGAACCTGCCGCTGCTAGAGCCACTGCGAT  
CGGTGCCGATCGTGGGGANACCCACTGGCGAACCTGGGTTCAACCAAACCTGAAGGTGATTGTTAACCTGGGCTACGG  
CGACCCGGCCTATGGTTATTGACCTCGCCGCCCAAATGTTG

## Clone Rv164

:::Rv164SP6.seq:::

AGCTTCCCGAGTTCGGCTTTGGATCAAGACCCAGTCCGCGGGCGCGATCCGGCNGCTCGGTGACTACATCAAGCCAC  
AAATCGACGGCTTTTCGGGGTCCGATACCGATGACGTGGCGGATGTCGAGTGTTGAGTTCTCGGCGGGGCGGATGCTC  
ACCTGGCGATCACCTGCCTCTCGTTGACGATCGATCGTCTATGCCGCCGTCTCTGCGGGAACAGGCCNCCAGTACATC  
GCCACAGACGGGATCCACCCGCATTTTCGGCTACGGTTGCTCGTTTCGGTGTTCGGACTAGTCGGTCCTGGTGACGTGC  
CGTGATGCGGACCGGTCTAGCACTGACCAATGGCCAAATGCGGGC

:::Rv164T7.seq:::

CGGGGGGCTCTTAATAGTGTAGGAAGAAGCTCTACATATTCAGGAGGATTACCATGGCTCGTGCGGTGCGGATCG  
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GGACCACCCCGTCAATTGTGCGGTTCCGCCGCAACGGTGAGGTGCTGGTCTGCCAGCCCGCCAAGAACCAGGCAGTGA  
CCAACGTGATCGCACCGTGCCTCGGTCAAGCGACACATGGGCAGCGACTGGTCCATAGAGATTGACGGCAAGAAAT  
ACACCGCGCCGGAGATCAGCGCCCGCATTTCTGATGAAGCTGAAGCGCGACGCCGAGGCCTACCTCGGTGAGGACATTA  
CCGACGCGGTTATCACGACGCCCGCCTACTTCAATGACGCCAGCGTCAGGCCACCAAGGACCCGGCCAGATCGCCGG  
TCTACGTGCTGCGG

## Clone Rv165

:::Rv165SP6.seq:::

ATACTCAAGCTTCATAACAGGCCTGTTGTGGGCGCACCCGGCTCGCCGAGTTCGCACGCACCGCCTCAAGTGCGGGC  
CGCACCGCCGGCATCTCCCGGTACGCGAGGGCCGCGGCCCGCGCCGACGCGGCGTGTTCGCGCAGTTCGCGGTCA  
ATGATGCTGACCTGATCGGCCACCCGGGCGTTCTCGGCGTCTTCGCGTTCACTAATCGCGGTGCTCAGCAGCGTCTCG  
ACAGCCACCACCCGAGTGGCGACCAGCTGCTCCACCACGACCGCAGCGATGCCGTACCTCACCCGTCCAGCGGTCC  
ACCACGACACGGTCTGTCACCAGCGCGGGCATTCACCACCCAGGCGGTACCGCCAGGCCGATCGCCACACCCGCC  
ACCATCCCCGATGCAGCCAGGCCGGGAGTAAGA

:::Rv165T7.seq:::

CTGGTGCTGGACGGAGCCTAGTACAACCTTCTCTCCAATGCTCTTGCCCCGATCGCGGCGACCAGGATGACCCAGGAC  
ATCCTGCCGCCCCGAAGTACTGGAAAAGCTCACACCCGAGTTCGTGCGACCGGTGGTGGCCTACCTGTGCACCGAGGAG  
TGTGCCGACAACCCATCGGTGTACGTGCTCAGTGGTGGTTAGGTGCAGCGAGTTGCGCTGTTTGGCAACGACGGCGCC  
AACTTCGACAAACCGCCGTCTGTACAAGATGTTGCGGCGCGGTGGGCCGAGATCNCGGATCTGTCCGGTGCGAAATT  
GCTGGATTCAAGTTGTAGAACTAAAT

## Clone Rv166

:::Rv166SP6.seq:::

ATACTCAAGCTTTTCCGGCGTCTCCACCTGACCCAAAAGCGCAGGTGCGCCGCCAAACGGCCCGCTGGCCGCGCA  
ACTGGTCCGGCTGCGCGTGGCCGACAATCAGTAGCTGGACATCCGGAAACCGCTGCACCACCTTCGGCAGCGCGTCAA  
GCAAAAACGGCCATTCC

:::Rv166T7.seq:::

TTTCAGATCTCATTTTTATGACATGACTGGAGATCTGTCTAGATTGCAGCTCCTGTGAGCGTGGGTACCGGATTCAAG  
CCGGTTCGGTACGCGCGGTGGTACCGGCTTTGCGGCAGTGCTCGGCCTCGAGTTCGCGGATCGCGCGCAAGTGCGT  
TTCGCGCACCAAGATCGCGGCCTAATGGCCGGCGATGACCGCGATGACCAGCGGATCCAGGAAAAACCGTTCCAACC  
AGTGCTGGGCGGCCATCCCCG

## Clone Rv167

:::Rv167SP6.seq:::

ATACTCAAGCTTCCCGACCACAAGTTGAACAGCACCGATTTCGGCGAGCACTTCGTCAACTTCCAGGGTGCCCGCACC  
AAGTATTTTCGACAAGTATTTCCGTGCGGCGCGCGCGCGCGCGGCGAGGTGGTCATCCTGGCGGCGGGGCTGGAC  
TCCCGCGGTACCGGCTGCCTTGGCCCCGACGGGACCACGGTTTTTGTAGCTGGACCGCCCGAGGTCCTTGATTTCAAG  
CGCGAGGTGCTCGCCAGCCACGGTGCCCAACCGCGCGCCCTGCGCCCGCA

:::Rv167T7.seq:::

GTGTGCTGTCAATTACAGAGCTGAGCCTGATGCACTCAACTACTGAGCATGCTAACGCTGGTTCGTGCGGGTCTTGTTTC  
CCGCGTGTGCGGAGGGCACACGCTCGGGGCGTAGCTGGGAGAGGCCCGGTCAAGCCCGAGAGCAGTGCTCAGTCCG

CCAGCTTGACCGACTTTTCGATGAGAACGCGCTTCTCGCCGTATTGAACTGGCGTGCTGACGGTCGCTGAGCAGCGCTC  
GCCGAGTGCGGCCGCTGATTCTTTCATCGAGCCAGGAGGCGCATTCTGTTCGGCCGCTGCGGGTCGGCCCCATCGT  
CGACGCGATCCGTCACCCACTCTCGATCAGGTCTGCCTCATCGAACGGGCCAACGGTGCTGTGGAGTATGTGTGCG  
TGGGCACGCGAGCCGGGTGCTGTGGTACACCACCGTTGCATGACCAAGTTGACGCCTGACTGGCTGAGCACC CGA  
TCCGCTCACAGGTGCGAACGTTGGTG

## Clone Rv169

:::Rv169SP6.seq:::

ATACTCAAGCTTTTGGTCTAGCCGGCCGAGCCCGATACAGGTGTCAATTGGCCACCGGCGGCGGTGTCCGGGAAATGG  
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CAGCGCGAAACTGAATCCTCCAACCGGGTTGTGATCCGGACAGGTTGGGGTGCGTTTGGGGCAATGACAGGTGGCGG  
CGGTGCGTCCGGGTGCGCCGGCGGAAGTGCTGCGTTGGGATCGCCCCGGCTGGGCATTCTGCGTGTTGGCGGCGGCCG  
TGTTGGGGGGCAACAGGTGTCTCGGTGCGGGTGGCGCTGCACC

:::Rv169T7.seq:::

GGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCGCCGACTTTCCGCGGTAC  
CCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTTTCATCCTGACGCCG  
GAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACTACATCATTTCGCACGGAG  
AACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGAACCCACTGGCGAACCTGGTTCAACCAAATTG  
AAGTGATTGTTAACTGGGCTACGGCGACCCGGCCTATGGTTATTTCGACCTCGCCGCCCAATGTTGCGACTCCGTTT  
GGGTTGTTCCAGAGGTGAGCCCGGTCGTATCGCCGACGCTCTCGTCGCCGGGACCCAGCACGGAAT

## Clone Rv16

:::Rv16SP6.seq:::

TTCTNTCTTCCCNATTCTGNNNTCTCNTACTACNCGGGCCNCAAAACACCTTGGCNAACGCTCAAAGGCGNTACNGG  
CACCAAGGCCCCACACGTCAACCTGTGACCTCCTGCGCCGACCCCGCCGAGGTCTGGCCGTTACCACTGAACGGG  
GAGCCGGGAGTCTGGTACGCATCGAACAAGAGCAAGGTGCATGGGCGGAGTTGTTCCGCCNCTTTTTTTATGACGGG  
GTGATCCATTGAGGTCCGTGCGCCGCTCGGTGAGTGGCGGTCACTCCAGGTACTCGACCTCNCAGACGAGAGG  
ACTCGATCCCATCTANGTGTGGACNAAACAGATCTTCTGTCCGACGACTACACACCACCCAGGCCATCGCCGCGGCC  
GCGATGCCAACTTCNACNCCGTNCTGGCCCCGGCGGCGGCGCTCCCCGGTTGTCAAACACCTGCCGTGTTCTGTTACN  
CACTGCCCAACATCNAGCCCGANCNATCCNAGGTCCGTCCAACGCCCTCCGCGGCTCNCAACCTNCTCCCNCTGATCN  
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:::Rv16T7.seq:::

CCGCTATCGGTGCGGTGTGCTTGGCGGCGTCGGTATCAACACCGCCACGAAATGGGGCACAAGAAGGATTGCTGGAG  
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CGGGTGTCACACCGGAGGACCCGGCGTCGGCGCGGTTCCGGCAGACGTTGTGGGAGTTCTGCCCCGAGTGTTATC  
GGCGGCTTGCCTCGGCCGTTCAATTTGAGGCCCAACGGCTGCGTCGGCTCGGCGTCAGCCCTGGAATCCCATGACG  
TATCTGCGCAACGACGTGCTCAACGCGTGGCTGATGTCGGTGGTGTGTTGGGGTGGGCTGATCGCGGTCTTCGGCCCC  
GCGCTGATCCCGTTCGTATCATCCAGGCAGTCTTCGGCTTCAG

## Clone Rv170

:::Rv170SP6.seq:::

ATACTCATGCTTGCCGAAGTTCGGATGGGTGCGCGCGGCANCCAGCGAAGTCGCTAGCGTGGCCGTGTTCTTGGCT  
TCGGATCTATCCTCGTACATGACCGGCACCGTGTGGACGTGACTGGCGGCCGTTTCATATGACACCGAGATCATTGC  
CACGGTACGGCAATTCGTCAAGAAGGAAATCTTTCCCAATGCACCGGCCCTCGAACGTGGCAACAGCTACCCGCAAGA  
AATCGTCGATCGGCTGGGTGTTATTGGCTTGTGCTCGGTGCGCGGCTGCAAGGGTATCGACACCACCGAGTTCATTCTCC  
GGCGTGCC

:::Rv170T7.seq:::

GGCGTCAACGGTGTGCGCACCGGCTCCTGCAGTTGGTAGGCCTGCAGTTTGTGCATCAGGCCGATGCCGCGGCCCTC  
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ATCGCAGCGCGGTGACCCAAACACATCGCCGGTCAAGCACTCCGAATGCACCCGGACAGCAGTCGTACCGTTCGGC  
GTTGGGCGCGGATCTCGCCGCGGACAGCGCGACATGTTCCAGTCTCTAGATGCTGGTGTAGCCGATGGCGCG  
AATCTCCCATGACGAGTCGGAATCCGCGCCTCGGCG

## Clone Rv171

.....:Rv171SP6.seq:.....:  
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TCCTTGGCGTCGACTCTTGTGGCAGCCACCGAGCGGTTGGTCCAGGATCTGGATGGGCAAAGTTGTGCGGCCCGGCCG  
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CGTCACCTCAAGCATTTCAATGGTTAT

.....:Rv171T7.seq:.....:  
ATGCGTCACCCCGATGCGCCAGATCGGGGCTTCGCAAATAAAGCACGAACAGGCGGGCAAACGTCTATCTCGGAGC  
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CCGGGCACCGGCCCGGGCTTTGGGGTCCNTCCGA

## Clone Rv172

.....:Rv172SP6.seq:.....:  
ATACTCAAGCTTCAATCGCGCCGCCACAATCCAAATATGCGTCTAGCGTCTCGATGAGCGTCGGTCCGGCATCGGCTA  
GGGGCCGCATCACGTCGGTATGCAAGGCCACGATCGCCCAAGGCGTCGCCCATCAAGGGCGCGTTCGGGCAAAAATTC  
CCCTATCCAGCACGGGCGCGCGCTCCGCNCCAGCCGGCGACGGCGTTTCATCCCGGAGATCGCCTCGCTAGCGCTGC  
GGTGCGCCGCGTCAAGATGGGCGCCGTGGGGCCGATGACCACCGGGGCGT

.....:Rv172T7.seq:.....:  
TTCGGCGGGTCTGTAGATTGCGGTGCGCCACCCACAGGCACTCATGAACCGCAGCCCACGATCGATCTCGGTGG

## Clone Rv173

.....:Rv173SP6.seq:.....:  
GCGCACCATCGCCAGTAGGTGCCCCGTGGTGGGGCGCGTCGAGCCACCCGAGCGGAAACGCGAGTCCGAACAGCAACAG  
CAGGACGGGCGCAACCAGGGCGGTGACCATGCCCCCGCGCTGAACATCAACCACAGGAAGGGCTCCGCCGAGCGTCC  
GCGCGACC

.....:Rv173T7.seq:.....:  
CATCGTCGAACCTTCGGTCCGGGTTGNTAGNACCGCAGCACCAAACGCACCCACCGACCCCCACGCTTCACGCCAACCC  
TTTAGTTTCATTGGCGTGAACAGCAGCGTAGCCGTTTGGCCGATATATGTGGAAAAATCGTTTCGGACGTACAAAAAAA  
GTTCTTGACGCTGGCGTCAACTCGAAACTGCCTCGGAAGTCAATGATGATCCATCAGTCAATATTAAAGTCG

## Clone Rv174

.....:Rv174SP6.seq:.....:  
ATACTCAAGCTTGTCTGCTGCCTCAGCGTATGCATCCAACAGCGCATCGCGATCAACGATCAGGCGCGCCGATTTCCG  
GCCGCGGGCAGTGGCACTGGCCGATGGCCGTTTTTTTCGAGAACTTCAACGCCTGAGCGCTGCTTCCCATCGAGAG  
ACCGGTGGCCTCTACAACCGATGCGACAGTTGGACCGGCGATGTTGCCAGCAGCGCTTACATACGGCAAGTNTGGC  
GCGG

.....:Rv174T7.seq:.....:  
TTGTCCAGGCGGGGAATCGGGCAGGAGACGACACCTTCGTTTCGGTTCGATCGTCGGAACGGGTAGTTGGCCGCGAC  
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CACAGA

## Clone Rv175

.....:Rv175SP6.seq:.....:  
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CTCGCATTTGCTGGCCTGGGTGCTGACCCNCCGNCNACAACACCGGTGGGTGGGCTGGGCTACGGCCTGCTATTCCGC  
CTGGTGTCTACGTCTCGTTGTTGCCGTGGATCGGCGAGCTGGTGGGCCCCGGGCCCTGGTTGGCACTGGCGACGACG  
TNCGCGCTGTTCCCGGCATCTTCGGTCTGTTGCGCCGCTGTTGACCTGTTGCCGGGTTGGCC

.....:Rv175T7.seq:.....:  
CGCCAATTACGATATCGTTAACCGATATCCCGAGCCGATAGCTGGCGGGCTCGGGTGGTGGCCAGCGGCGCTGCGAC  
GAAAGGTGTGACCGTCATGAAACAGACACCACCGCGGCCGTCGGCCGTCGTACCTGCTCGAGATCTCAGCATCCGC

AGCCGGTGTGATCGCGCTTTTCGGCGTGTAGTGGGTGCGCGCCGACCCCGGCAAAGGCCGGCCCGACACAACCCCGGA  
ACAGGAAGTCCCGGTACCGCGCCCGAAGNACTTGATGCGCGAACNCGGAGTGCTCCAAACGCATCTGCTGAT

## Clone Rv176

:::Rv176SP6.seq:::

ATACTCAAGCTTGGGCACTGACTTCGGTACCCCTCCGCTTTGGCCAGCAGCAGCCACAGCGCGTTTCGCGGACCGA  
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TAGTCTTGGGCCCCACACCCACAGTGCTTCGACGGTACGGTCACCCATGATGGCCATCCAGTTGGCATCGGTGAGCT  
GATAAATGCCAGCTGGTTTCGCCAACCCGGTAGCGATCTTGGCGCGCTGCTTGTGTCACTGATACCTATCGAGCAAG  
ACAGCCCGGTTTGCACAAAATGACTTTTCGGATCTCTTCGGCGACTTCGATGGGGTTCGTCGGGA

:::Rv176T7.seq:::

AAAGTCCTGTGCCGTTTCGCTAAACACCCGGCGGACACTCAGACGGTGCTGGTGGTGGCGCATGGCACCGCGGGCAGC  
AAAGCGCACTTCTCCGGGGGACGACAGCAAGCGACCGCTAGACAAGAGGGGTCTGCGCAGGCAGAAACGTTGGTACA  
CAGCTGCTGGCGTTTCGGCGCCACCGATGTTTATGCCGCGACCGGGTGCCTGCCACCAGACGATGGAGCCACTCGCC  
GCGGAAGTGAACGTGACCATAACA

## Clone Rv177

:::Rv177SP6.seq:::

ATACTCAAGCTTGGGTTCACGCCCCGCGCAGCCACGCCGTACCTTTCCACGAGACCTCACCTGCCGATCCGAAATGG  
AATCGGCCGTGACGGAATTGGCGCACCGAACACCCAACGAGGTGGTGGCTTCGTCGCGAACCGTCACCCGAGTCGCGG  
CCACCGTGCGCACGGCGACGTTCTACACCCGCACCAAGATCCGAAAGCTGCAAGCTCCAGCACCGATCCCGACGTCA  
TCACCGCTGCCGCCCGGCACGTCTTGACCTATTGAGCTGGATCGGCCCGTCCGGTTGCTGGGAGTGCGGTTAGAAC  
TGGCCTAGAACCGCGGGCACACCGCNCCTGGGCGGGGCGAATTCTTGACCGCNCGGCC

:::Rv177T7.seq:::

CGCGGTTGGCGTAGTTGGACGGTTCGCCCTCCGAGGCCAATGATGACGATGACCACGCCGATCACGATGGCCACCGAG  
AGGGACAACAACAGAAAGCTGACGAATCCCTCCTTGGCGGCCGGGGCTTTGTGGTCCGCCGTCGCGATGGGCGCGAAT  
TTACGGCCCGCTCCCCAGGCCCGCGAAGCAGGGTCCCCAGCCAGTTGGCGTAGGCGGAATTAACGATCAGCGCCA  
CCGCGATAACCTGCCATGCCTCGGGCATATCGATGTGCGGCCAGAACAGGCCGAAC

## Clone Rv178

:::Rv178SP6.seq:::

CCAACAAGAGCATCGGGACATACGGAGTCAACTACCCGGCCAACGGTGATTTCTTGGCCGCCGCTGACGGCGCGAACC  
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CGGCCGTGATCGACATCGTCACCGCCGACCACTGCCGGCCCTCGGGTTACGCGAGCCGTTGCCGCCCGCAGCGGACG  
ATCACATCGCCCGCATCGCCCTGTTCCGGGAATCCCTCGGGCCGCGCTGGCGGGCTGATGAGCGCCCTGACCCCTCAAT  
TCGGGTCCAAGACCATCANCCTCTGCAACAACGGCGACCCGATTTGTTGACGCGCAACCGGTGGCGAGCGCACCTAG  
GCTACGTGCCGGGATGACCAACCAGGCGGCGGTTTCGTGCGGAGCAGGATCTAACCGCGAGCCGCCCATAGATTCC  
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:::Rv178T7.seq:::

TAANACCCGTGTAATTTGGGATGGGCAAAAAGGCCAAGCACCGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGC  
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GGATGGCAGCAACCTGGTAGCNCCTGGCCGGGCGATGATCTGCAGCGTCGCCGCGGGTAGTCGCCGCCGGGCGGCT  
ACAGTCTGAAACGCGATGACCATCGATGTGTGGATGCAGCATCCGACGCAACGGTTCCTACACGGCGATATGTTCCGC  
TCGCTGCGCCGGTGGACCGGTGGGTCTATCCCGAGACCGACNTCCCGATCGAAGCGACCGTCTCCTCGATGGACGCC  
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## Clone Rv179

:::Rv179SP6.seq:::

GTCCGCAAAAGACTCAGCGGCCGACTTTGCTCGCAGCTGGCGGTACCGCGCCACCGATTTCGATGCCGTGGTCGCGGAA  
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CACGGCACCCACATGCGGCAGTTTCGTCCACCTGGGCCAGCGCCCCGCCCGGAAGTCCAAACAATAGAAGTGCACCCG  
GCCCCGATCGTGGGTAGCAGCCAACGCCATGATCAGCGTCCGCGAGCGGGTTGACTTGCCCGTTTGGGTGCACCTAC  
GACCGCGACATTGCCTGCGGCCCGGACAAGTCGATCGTCAGCGGCACCN

.....Rv179T7.seq:.....  
CGTGGCCACGAACGCCGGGAGGGACANTCTCGGGCGGCTAGGGCTTCTCGCGGGAAGGCCCGAACGTACGGCGTTTCA  
ACACGTTCGCGTCGCCCTCCGACCGCAACATTGCGGGATGGCAGCAACCTGGCAGCTACCTGGCCGGGCGATGATCTG  
CAGCGTCGCCCGCGGGTAGTCGCCCGCCGGGCGGCTACAGTCTGAAACGCGATGACCATCGATGTGTGGATGCATCATC  
CGACGCAACGGTTCTACACGGCGATATGTTTCNCCTCGCTGCGCCGGTGGACCGGTGGGTCTATCCC

## Clone Rv17

.....Rv17SP6.seq:.....  
ATACTCAAGCTTTGCGGGCGGGCGCCGAAATGTGAACGCACCAACCCGCGCTGCGGGTTCGGCGGGCCACTCGACCT  
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CGCCGTCATAAAGCTCGAACAGCACCGAAACCGACTCCACCACCGGGCGGTGCGCCTCAAATCCACGCCGATCTCCA  
CATACCGGGAACAGTCGGTGTCCCATCGGGTTTCGGCTTGCCCGCCAGCTGCACACCACCGGTGGCCTCGGCCACCT  
TCGCGGCCTGAGCGCAGCTACNCATCCTGACGATCATCACCCGCCCGGCTCACGCTTGCCCTCCGTGACCGCAGC  
CATCGCCCGGTTGCGCGCACCGCGACGCCCGTACAGCCGCGCGCAC

.....Rv17T7.seq:.....  
AGCTTGCCGGGACTGCGGAACAGAAGCGGCGGTTCTACCGCGGTGTGCGGCCGGCGCGATATCGGCCTTTTTACTAA  
CCGAACCCGATGTGGGCTCCGATCCGGCGCGCATGGCATCGACGGCGACGCCGATCGATGACGGCCAGGCTTACGAGC  
TTGAGGGTGTGAAGTTGTGGACCACCAACGGTGTGGTAGCGGACCTGCTAGTGGTTATGGCGCGGGTACCGCGCAGTG  
AAGGGCACCGAGGGGGAATCAGCGCCTTTGTCGTCGAGGCTGATTCGCCCGGGATCACCGTGGAGCGGCGCAACAAGT  
TCATGGGACTGCGTGGCATCNAACCGCGTGACCCGGCTTCATCGCGTCNNGGTGCCCAAGACAACCTTGATCGGCA

## Clone Rv180

.....Rv180SP6.seq:.....  
CTCAAGCTTGCGGATGCGGGCTGGCCAAACTGGCCGGGCGGGGTTGGCTTGTTCAATCAAGGGTGGGTTGCCG

.....Rv180T7.seq:.....  
CCGAAGGCCCGTTCCCGGGCGTTCAGCAAGCGATCGTCGGTTGGCCACTGCGGGTTCGAATCTTGCGGCCGCGCCGGT  
CGTGGAACGCCCAGGTCACCCGGCGCGCTACC

## Clone Rv181

.....Rv181SP6.seq:.....  
ATACTCAAGCTTTTTTCTGCTCATGAAGGTTAGATGCCTGCTGCTTAAGTAATTCCTCTTTATCTGTAAAGGCTTTTT  
GAAGTGCATCACCTGACCGGGCAAATAGTTCACCGGGGTGAGAAAAAGAGCAACAACCTGATTTAGGCAATTTGGCGG  
TGTTGATACAGCGGGTAATAATCTTACGTGAAATATTTCCGCATCAGCCAGCGCAGAAATATTTCCAGCAAATTCAT  
TCTGCAATCGGCTTGATAACGCTGACCACGTTTATAAGCACTTGTTGGGCGATAATCGTTACCCAATCTGGATAATG  
CAGCCATCTGCTCATCATCCAGCTCGCCAACCAGAACACGATAATCACTTTCCGTAAGTGCAGCAGCTTTACGACGGC  
GACTCCCATCGGCAATTTCTATGACACCAGATACTCTTCGACCGAACGCCGGTGTCTGTTGACCA

## Clone Rv182

.....Rv182SP6.seq:.....  
CTCAAGCTTGGTGCCGACATGGCCGGGCTGGAGCCCGCGTATGGCAAGGTTCCGCTCAATGTGGTTGTGATGCAGCAG  
GACTACGTTTCGCTCAATCAGCTCAAACGTCACCCCGTGGCGTGCTGCGCAGCATGAAGTTCGGCGCCCGCACGATG  
TGGGCGAAGGCAACAGGTAACAACTGGTCGGCATGGGTTCGAGCCCTCATTTGGGCCGTTGCGGATCGGGTTGCACCGC  
GCCGGAGTGCCGGTTCGAATCAACACCGCCTTCACCGATCTTTTCGTCAAAAATGGCGTCGTGTCCGGGGTATAC

.....Rv182T7.seq:.....  
CCGAAGCGTGGGAAATCCTGACCGAATACCGCGACGTGCTGGACACTTTGGCCGGCGAGCTGCTGGAAAAGGAGACCC  
TGCACCGACCCGAGCTGGAAAGCATCTTCGCTGACGTCTAAAAGCGGCCGCGGCTCACCATGTTGACGACTTCGGTG  
GCCGGATCCCGTCGGACAAACGCCCATCAAGACACCCGGGGGAGATCGCGATCGAAACGCGGCGAACTTGGGCC

.....Rv183SP6.seq:.....  
CGACTCGACAAGCATTCTTGACAGTTGTTTTGGCTCGGCATGGTTAGCCAAGGTTCTGCGGTCCCACCAGATCATCTT  
GGTCCGGTAGCGCTCGTCCGGGTATGCTGCCGCCGGGATTCGCTGCTATTACTCCCCCGAAAAACGCCACCGGTC  
CAGCGCGTGGGCGCCGCGGTCCCCATCACAACCTGAACCCCAACAGGGGACATGCTTAGCGGTAGGGCGCGCGCCA  
AGGCGGCAGCAATCGCATCACTGCGCTGCGGTCCTATTAACCCACCCGGACTTCACTTCCACGACCCCGAATGGCG  
CCCGGTCATTGATCATCTTGCGCACCGCGGATAATCCGGGATTGCCAGCCCATTCGACTACCGCATCGAGTCATCGG  
CTGACCGCAGCGGTCCGATTACCCGAGCGCCCCGANTACATCTCCTCCAATATCAATGGGCGCAA

## Clone Rv183

:::Rv183T7.seq:::

GCGGTNTAGCTTCCCGTCGTACCGGCGACCGCCAGCCGAGAAGCTCGTTTTCCCAGTGTGCTGGGGATTCTCACGCT  
GCTGCTGAGTGCGTGCCAGACCGCTTCCGCTTCGGGTACAAACGAGCCGCGGGGCTACGATCGTGCGACGCTGAAGTT  
GGTGTCTCCATGGACTTGGGGATGTGCCTGAACCGGTTACCTACGACTCCAAGCTGGCGCCGTCTCGTCCGCAGGT  
CGTTGCTTGCGATAGCCGGGAGGCCCGGATCCGCAATGACGGATTCCATGCCAACGCTCCGAGTTGCATGCGGATCGA  
CTACGAATTGATCACCCAGAACCATCGGGCGTATTACTGCCTGAAGTACCTGGTGCGGGTCGGATACTGCTATCCGGC  
GGTGACGACCCCCGGCAAGCCGCCATCCGTGCTGCTGT

## Clone Rv184

:::Rv184SP6.seq:::

CTCAAGCTTGGGCGTGACGGCCACCGGGGCCACTCCGACAATCTGTACCCGACCAAGATCTACACCATCGAATACGA  
CGGCGTCGCCGACTTTCCGCGGTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCA  
CTCCAATACTTTCATCCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGAC  
CCAGTACTACATCATTCGCACGGAGAACCTGCCGCTGCTAAAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACT  
GGCGAACCTGGTTCAACCAAACCTTGAAGGTGATTGTTAACCTGGGCTACGGCGACCCGGCCTATGTTTATTCC

:::Rv184T7.seq:::

CGGGTGTCAATTGGCCACCGGCGCGGCTGTCCGGGAAATGGCGGGTCCCCGGTGGTTTTGCTGAGGAGTGCTGAACCG  
TAGTCGAAGTGGGCGGCGTCAGACTCCACCCAGCCAGCAGGCAGCGGAAGCTGAATCCTCAACCGGGTTGTGATC  
CGGACAGGTTGGGGTGCGTTTGGGGCAATGACAGGTGGCGGCGGTGCGTTCGGGTGCGCCGGCGGAGGTGCTGCGTTG  
GGATCGCCCGGCTGGGCATTGCGCGTGTGGCGGCGGCGGTGGTGGGGGGGCAACANGTGTGCGCGGTGCGGGTGGC  
GCTGCA

## Clone Rv185

:::Rv185SP6.seq:::

NCTTGATATTGGCGTCAACGGTGTGCGCACCGGCGTCTGCAAGTTGGTAGGCCTGCAGTTTGTGCATCAGGCCGATGC  
CGCGGCCCTCGTGGCCACGCATGTACAGCACACGCGCGCCCTCACGGGCGACCATCGCCAGCGCGGCGTCCAGCT  
GAGGCCCGCAATCGCAGCGGCGTGACCCAAACACATCGCCGGTCAAGCACTCCGAATGCACCCGGACCAAGCAGCTCGT  
CACCGTCGGCGTTGGGCCCCGGCGATCTCGCCGCGGACCAAGCGGACATGTTCCACGTCTCGTAGATGCTGGTGTAGC  
CGATGGCGCGAACTCCCATGACGAGTCGGAATCCGCGCCTCGGCGACCCGCTCAATGTGCTTCTCGTGTGCGCC  
GCCATTGATCAAGTCAGCAATGGTGATCAGCGCCAGACCGTGCTCNTCGGCG

:::Rv185T7.seq:::

CATAAGGGCCGGCGTACCCGGTACCGGCCGCGGGCCCTACCAGTGCCGGAAGTGAAGCGCAGTAAGCCCTCAACGCG  
CCACCGCTTTGGCCCGCGCGCCCGGCGTAGGCGCATCGGCGGTGGCCGTGGGGCGGCGCACTGCGACCTCACCAGCGG  
CTTTCGAGCTTTGTTGATCAACCGGCCAGCATGGTCGAGGATCGATTGAGACCATATTCGAAATTGGTTTCATCGG  
GGGCCCCGATCCGATGCCCCCTCCAGTTGCGTGAGCAAGCAGCGGAGTCGTGCGGGGATCGATGGCCACGGGGTGT  
CAATGGCGGATGGTCCGCTGCCCGCCGACTGGCTCTTGCGGGAGAGCCGATCTAGCACCACCGATCCGCGCACGTGGA  
CCGAAACCGCCGAGTAGATGTCGAAAGCGT

## Clone Rv186

:::Rv186SP6.seq:::

CGTCCTTTTCCCCAAGATAGAAAGGCAGGAGGTGTCTTCTGCATGAATATGAAGATCTGGTACCCATCCGTGATACA  
TTGAGGCTGTTCCCTGGGGTTCGTTACCTTCCACNAGCAAAACACGTAGCCCCTTCAGAGCCNNATCCTGAGCAANAT  
GAACAGAACTGAGGTTTTGTAAACGCCACCTTTATGGGCAGCAACCCGATCACCGGTGGAATACGTCTTCAGCAC  
GTCGCAATCGCGTACCAACACATCACGCATATGATTAATTTGTTCAATTGTATAACCAACACGTTGCTCAACCCGTC  
CTCGAATTTCCATATCCGGGTGCG

## Clone Rv187

:::Rv187SP6.seq:::

CTCAAGCTTCATGTCCGTACGGCTCGGGTACGCTTCCGTGCGAGTGTGCGAGTGATAAATGACGACCGGGACCTCGTC  
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GGTCATCGGGATATGCCGCTCGGGACGGTCAGAGCCCTCGGGTCCGGCCAGCACTCCGAGGCTTCGTGCGGGTGGTC  
GCGACACGCATGGGCCACCATCGCATTAC

.....Rv187T7.seq:.....

NCGCCGCCAGCCACCACGCGCGGGTCGGGCGCGGGCCCGGGCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACC  
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CTTTCGAGGTCGAGGTCGATACCGATTTGCGCATCCGCAGCCGCACCCTGGACGACAGAACCGTGCCCTACGANTGCT  
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TTCCGGTGCTGAT

Clone Rv188

.....Rv188SP6.seq:.....

CGCCACGTTTCATGGGCAACAACCCCGATACCGGTGGAAATACGCTTTCAGCACGTCGCAATCGCGTACCAAACACAT  
CACGCATATGATTAATTTCGTCCAATTGTATAACCAACACGTTGCTCAACCCGTCCTCGAATTTCCATATCCGGGTGCG  
GTAGTCGCCCCTGCTTTCTCGGCATCTCTGATAGCCTGAGAAGAAACCCCACTAAATCCGCTGCTTCNCCTATTCTCC  
AGCGCCGGG

Clone Rv189

.....Rv18SP6.seq:.....

ATACTCAAGCTTCAACCGATTGACGCATTGTGCGAACTGACGGCGCCCCGCGCATGGCCAATCCGGAAGACCATCATTG  
GCCAGTGGCCGGGCGCTAACAGGTTCCAGCCCCCACCAGTGCCGCTCGAACATGCGGTGCAACCCATTTCGAGGCCG  
GCAGGAAAGCACCCGCGGAAGCCGCAAGGGCTGCAGTTCGCGGCCCAATAGTGTCTGTCGCAACCAGATGCGCTCGA  
AAACCGCGCCGGCAGTCAGCGCACCCGACGCGAGGTGAGAGACGTCGTCAGCGCGCCACATGGGGTGCCAATCGGC  
ACGGCAGGTAGGCCGCGCGCAACCCGAACGCGTGGTGCATGCCACGGTCCGCGAGGAGGCGCAGCACCCGCCAATGCC  
GAAGCCACGAAACATCGGGCGCATCCACGCTTCAACCTC

Clone Rv18

.....Rv18T7.seq:.....

AGCTTTTGGCAGGGTCTCCTTCGAATTCGGCGTGCACCGCTATGGGTGTCAGCAGCGGTGGCGCCGCACACCCCACT  
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CCGCGAGGCCATCGACCGATTACTCGCCACCGGGGTGCGAGAGGTGCCGCGATCCCGTCCGTCGACGTCCTCGACGA  
TCCATCCGGCTTCCGCCGTCGGGTGGCGGTAGCCGTCGATGAAATCGTGCCGGCCGCTACCACAAGGTGATTCTGTC  
CCGTTGTGTCGAAGTGCTTTTCGCGATCGACTTTCCGTTGACCTACCGGCTGGGGCGTCGGGCACAACACCCCGGTGAG  
GTCGTTTTTGTGCGATTGGGCGGAATCCGTGCTCTGGGTTACAGCCCGAATCGTCAC

Clone Rv190

.....Rv190SP6.seq:.....

ATACTCAAGCTTTGTACACCAACTGTTTCCACAGGCGCTCCATCCGGCGAGTGGATACTCCAGCAGGTAGCAGGT  
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CAGCTTGGGGATCGCGACTTCTATGGTTGCGGACAGGGGTGTCGAAATCACGGTGGCGGTAGCCGTTGCGCTGATTGGA  
CCGCTCATCGCTGCGTTTCGCGGTAGCCCGCCCCGCACAGGGCGTCGGCTTCAGCCCCATCAAGGCGGCGATGAACGT  
CGAGAGCAGCCCGCGCAGCAGATCCGGGCTCGCCTGTGCGAGTTGGTCAGCCAGAACCTGCTCGGTGT

.....Rv190T7.seq:.....

CCTTAAGCCCCGCAGGGCCCCGCACGCGCGGTACCGCCCAACAGATCGTCGATGTTCCGCTCGTCCGCC  
TCGCGCACGTGGTCTGTACCAAGTCAACGTTAACGCCGCGCACATGTCCTGCGGCCGGGCAAAAACGTGAAAAACGA  
TCCGGGCGACTGCAATGTATGACACCGACGGCCCGGATGGGCCAGGGTCTGGCAGATTCGATCTGTGCGGCCAGTG  
CCAGCAGCGTCGCTTCGTATACGGCCGCGCCGACGAGTTGAACCGACATGGGCAGGCCGTCGCCGTCGAAGTCCCACG  
GCACCACGGCCGCGGGTGGCCGGTCAGATTCAGACTTGAAAGTACGGAACCCGCTGCACCACAGCAGCAACGTCG  
AAACTGCACCCCGGCGTTGGTAGGCGCGATGCGGGACGGGCGGTCGCGGCGCCTGGCGTCACAACCTACGTCGACAT  
CGTCGAAGATCGACTGGATCGGCTGCTCACACCACTCGGCGGCCGAGGCCGCCATCCGCCGTC

Clone Rv191

.....Rv191SP6.seq:.....

AGCTTTTTTGAAGCTGCGCGGGGCGAGCTTCGCCGCAATTCTACTAGCGAGAAGTCTGGCCCGATACGGATCTGACCG  
AAGTCGCTGCGGTGACGCCCACCCTCATTGGCGATGGCGCCGACGATGGCGCCTGGACCGATCTTGTGCCGCTTGCCG  
ACGGCGACGCGGTGGGTGGTCAAGTCCGGTCTACGCTTGGGCTTTGCGGACGGTCCCGACGCTGGTTCGCGGTTGCGC  
CGCGAAAGCGGCGGGTGGGTGCCATCAGGAATGCTTCACCGCCGCGGCACTGCACGGCCAGTGCCCGCGGCGATGTCA  
GCCATCGGGACATCATGCTCGGTTCTACTCTCGACCACTCGGCGGAACAGCTCGATTCCCGGACCGCCAGCGCA

TTGGTGATGGAATCGGCGAACTTGGCCACCCGCTGGGTGTTGACATCCTCGACGGTGGGCAATTGCCCCCGGTAACGT  
TTGCCGCT

::::::::::Rv191T7.seq::::::::::

CGGTCCGACCTGTTTCGACGGCTACCTGAATCAACCCGATGCCACCGCCGCGGCGTTTCGACGCCGACAGCTGGTACCG  
CACCGGCGACGTGCGGGTGGTCGACGGCAGTGGGATGCACCGCATCGTGGGACGCGAGTCGGTCGACTTGATCAAGTC  
GGGTGGATACCGGGTTCGCGCCGGTGAAATTGAAACGGTGCTGCTCGGGCATCCGGACGTGGCGGAGGCGGACGTCTG  
CGGGGTGCCCCGACGATGATCTAGGCCAGCGGATCGTTGCCACGTAGTCGGCTCAGCGAATGTCGATGCGGACGGGCT  
TATCAACTTTGTTGCCCAACAACCTTTCGGTGCACAAGCGCCGCGCAGGTGCGTATCGTANATGCGCTGCCGCGCAA  
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Clone Rv192

::::::::::Rv192SP6.seq::::::::::

ATACTCAAGCTTGCCGAAGTTCCGATGGGTGCGCCGGCGAGCCCAGCGAAGTCGCTACCGTGGCCGTGTTCTTGGCT  
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CACGGTACGGCAATTCGTCAAGAAGGAAATCTTTCCCAATGCACCGGCCCTCGAACGTGGCAACAGCTACCCGCAAGA  
AATCGTCGATCGGCTGGGTGTTATTGGCTTGCTCGGTCGCGGGTGCAGGGGTATCGACACCACCGAGTTCATTCTCG  
GGCGTGCCGGCGCATTCGAGCTGGCGGTGCGCGCTGCCAGCACCGTCATAGGTACTTGACGATGGTCCACGTCGGAC  
GAGCGCTCCACGTGCTGCCGAACGGTATGCATGGCGGGTACGATTCTC

::::::::::Rv192T7.seq::::::::::

CGGTGTCGGCACCGGCGTCCTGCAGTTGGTAGGCCCTGCAGTTTGTGCATCAGGCCGATGCCGCGGCCCTCGTGGCCAC  
GCATGTACAGCACCCACGCGCGCCCTCACGGGCGACCATCGCCAGCGCGCGTCCAGCTGAGGCCCCGAATCGCAGC  
GGCGTGACCCAAACACATCGCCGGTCAAGCACTCCGAATGCACCGGACCGAGCAGTCGTACCGTCGGCGTTGGGCC  
CGCGGATCTCGCCGCGGACCGAGCGCGACATGTTCCACGTCTCGTAGATGCTGGTGTAGCCGATGGCGCGAACTCCC  
CATGACGAGTCGGAATCCGCGCCTCGGCGACCCGCTCAATGTGCTTCTCGTGCTTGCGCCGCCATTGATCAAGTCAG  
CAATGGTGATCAGCGCCAGACCGTGCTCATCGGCGAACACCGCAATTCATCGGTGTTGCGCCATCGAGCCCTCATCTT  
TTTGCTGACGATCTCGCAATCGCCCCCGCGGGTTCAGCCGGCAT

Clone Rv193

::::::::::Rv193SP6.seq::::::::::

ATACTCAAGCTTTGGGTGAAAGCCGATCACCGGAAGCCGCATGATCAGCCACGTTTCGCGCCGCGCGGCATACGGCGG  
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TGAATCGAGTTCCAGGTCCAGCGGGTGGCGCAGCAACGGCGCGAGCTCAACGACGTCAATCACGTTGTGCTTTCTAC  
GGTCAACGACCCGGTGACCGTNTCTGCCCCGGTGCGCTCGGCCGATAAGTTGCACCGCCACCACCGCGACACCGTCTTG  
CACGCGGACCCACCCCGGATCCGTTGTTGGCC

::::::::::Rv193T7.seq::::::::::

AGCTTGCTGGCATCCGCTCCAGTAGCGCCCCGCGCGTGGCTTCAGCGCCCGCAGATGCTCCATGAGCCGGCCGGTCG  
AGTCGGCGCCGGCGTTACCGCCACCCGCCAGGAGCTGGCGGCCAGCATCTCCGCCTTCACGCATTGCGCGATCACAG  
AGAGAATATACGTCTCATATTCGTTGGAGGTCTGCGAGGCAATCGGTGATGACGGATTGATGGCATCGAGCTGTG  
CTTCGGCGTAGCCCTCCAGCACGTGCGTATCGTGTGGCGGTCCACGACGACCGCACCAGCGCGCGGACAGCCGTCG  
GGTTGGACGNTGTGCGGCGATCAGTCCGGCCAGCTCCGCCTCGGGATCAGCGGC

Clone Rv194

::::::::::Rv194SP6.seq::::::::::

ATACTCAAGCTTGCTGCAGCTTCCTATGACTGCTCCCGAAACCTGGGGGTGTGCCTGCTGTATGCACGGCATAACGG  
ACATCCTTCCCTTGAGACCCGCGGTGCAACCAGCCACGTGTCCATCATCAGGGGTCAACCCCGGCCAAGGGCGACGGC  
ACGCCAAGTTCGCCGACCGTTAACCTAGTGCTGTTAGCTTCATTTGCTGCGAGCAAAACAGCTGGTTCGGCCGTTAGGA  
ACTGAATTGAAACTCAACCGATTGGTGCCCGCGTAGGTGCTTGCTGCGGGTGCCTGCTGTTGTCGCCGCTGTGGT  
AACNACNACAATGTGACCGGGGGAGGTGCAACCACTGGCCAGGCGTCGGCGAAGGTGATGCGGGGGGAAGAAGAAC  
TCAAAGCCAGTGGGTGACGCGCAGGCCAACGC

::::::::::Rv194T7.seq::::::::::

AGCTTGACGCGGAGACGGACACATTGCGAACATTGATGACAAAATAGAAATCATTGATGGTTTGAGTCACCAGGCCGA  
TCAAGCCTTCGCCGAGCCAAATCCAATCAAGAGGCCCAAGCCGTACCAATCAGCCCGGCAACGAGGGATTCCGTCA  
TTATCAGCCAAAATAACTGCTCTCGGGTTACACCCAAACAGCGCAATATGGCGAAAACGGTCGCCGTTGCACGACAT  
TAAATGTCACGGTATTGTAGATTAAAAAGATACCCACCAACAAGGCAATCAAATGAGAGCGGTTAAATTGACCGTAA

AAGCGTCCGTCATCTGTTTGACGGTGTCCCGTTGGGTATCCGACGTTTCCATACGCACACCGGCCGCGAGTCTTTGTT  
GGATGCGTGTTGCAGTGGCCTCATCTTTGATGATCAAATCGATGTGGCTCAGTCTTCCGGGCA

## Clone Rv195

:::Rv195SP6.seq:::

ATACTCAAGCTTCGGCTCAGGCGGCGCTGCTGGTAAAGTCGCTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTC  
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TTGAGCATGAGTCGGCGACCGTCGTTCATGGTCGACACCCACGACGGAAGACGCAGATCGCCGTCGAAGCATGTGTGCC  
GCGGATTATCAGGACTGACCTCCTGGCTGACCGGCATGTTTGGTCGCGATGCCTGGCGCCCGGCCGCGTGGTGGTGG  
TCCGCTCGGATAGCGAGGTCAGCGAATTCNCNTGGCAGCTCAAAGGGTCCTGCCGTTGCCGTTCTTTCGCGAAACNA  
AGGCNCAGGTTA

:::Rv195T7.seq:::

TGATCGCGCATCACCTGCTTCATAAAGTGAAGCAGCGCAGCGCTTCTTTTTCGGCCGCAACATGAGCCAGCCTCTCG  
TCGGCGGTCGGGTGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCTGAAACCAGCTTCCATATCCCGCG  
ACGAACGACGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCGTTCTCCACCGACCGGGCCCG  
GGTGTGGGGTGTTCGGCGACCGGCAGCCAGGTGGTCCACACTGCCGACGGGCGCCGCGAGCCGTTACCGACCGAGGC  
CGCCGAGCAAGTCCGCCCAGTCGCATACTCCAACCGGTTGCGGTACTGCAGGTTACAGTGGCGTACTCCTCGTCGCGC  
TCGGCGAGGTCTTGCTCCAGCACGTTCGANACGGCAG

## Clone Rv196

:::Rv196SP6.seq:::

CAAAGCGGAACTGCTCGCGGCAGCCACGACGTGCTGCGTCGGATTGCCGGCGGCGAAATCAATTCCAGGCAGCTCC  
CGGACAATGCGGCTCTGCTGGCCCGCAACGAAGGACTCGAGGTACCCCGGTGCCCGGGTTCGTTGGTGACCTGCCGA  
TCGCACAGGTTGGCCCAACCGGCCGCTTGATGCCCGGTGCGCAAGCCCGGAGTTGCCAAACCCAGCGTGATCAGG  
CTCGGCTCGCGAGTTCCGGGAAGAAGTGGCTCCGCCTGATCACCTACCATCCGCCAGGATCTGCGTGTCTTACCACG  
CCCGCCAAGGAGGTTGTTGTGGTGCTATCGACCGN

:::Rv196T7.seq:::

CCGGAAGCCGCATGATCAGCCAAGTTTCGCGCCGCCCGGCATACGGCGGCGTACCGATCTCCGCGTCATACACCCGCG  
GGTAATCGCCGACGGTGCCGGTTTCGCGAGCCGAAGGTGACGACGCTGATTGAATCGAGTTCCAGGTCCAGCGGGTGGC  
GCAGCAACGGCGCGAGCTCAACGACGTCAATCACGTTGTGCTTTCTACGGTCACCGACCCGGTGACCGTNGTCGCCC  
GGTGCCTCGGCCGAAAANTTGCACCGCCACCACCGCGAAACCGTCTTGACACNCCGGAAGCCACCCCGATCCGTTGT  
TGGGCCAGGTTATTGGGT

## Clone Rv19

:::Rv19SP6.seq:::

CCGGAACCGCCGACGGCACGCTATAACGCCTCCGCATATGGGTGCGACAACCAGCGGTCGGACTTCTGGGCTTCTAGC  
GTTTCGCGNGTCGCGACAAACAGCGCGGTGGAACCGACACTCGTTGTGATGTCCTAGCTATCACGTTCCGTTACGACCC  
CAATCGAGTCTAGCGCGGTAGNTCAGCCCCGATCTCCANGCTCCGCCGAGCCAGGCGC

:::Rv19T7.seq:::

CTGGTTTATGTCCCGTTGAAGTTCATCACCCGATGTGGCGGGAGCACTGCCAGGTGATCTCAACTACCACATCCGG  
CCGTGGCGGTTGCGCGCCCCGGGGGGTTCGGCGCGAACTCGACGAGGCGGTGCGAGAAATCGCCAGCACCCCGCTGAAC  
CGCGACCACCCGCTGTGGGAGATGTACTTCGTTGAGGGGCTTGCCAACCACCGGATCGCGGTGGTTGCC

## Clone Rv1

:::Rv1SP6D2.seq:::

CCGAGCAGTTGGGAATCGCTCTGCANCAAACCAATATTCTGCGCGACGTGCGCGACGAGCTGGACCGATTAGGCGTA  
CGCCTCCGNTGACGACACCGGGGCACTCGATGACCCCGACGCCTACGCTCGCAGGATATTGTTTCGCGGACCCCTC  
TCTAG

:::Rv1T7.seq:::

TATATAATACTCAAGCTTGCCGACGCCAACGCTCGCGCGATGTTGTTAGCCCGACCCGGCTCTTACATGGCACCGGTG  
CCCCACACGTCAGCCTGTGACGTCCTGCACCGCGACTCTTTACATAGAATGTGGATTGCCGGATTGGGGATGTCCGGC  
ATCGCTCAATCTGTAGTCCGCGTGTCCCGCGAGGGCCATGTGGATGGGGGGAAGGATCCGTGGCGTCCGGGATCACC  
ATGGGG

## Clone Rv201

:::Rv201SP6.seq:::

ATACTCAAGCTTGCCGAAGTTCCGATGGGTCGCGCCGGCGAGCCCAACGAAATCGCTAGCGTGGCCGTGTTCTTGGCT  
TCGGATCTATCCTCGTACATGACCGGCACCGTGTGGACGTGACTGGCGGCCGGTTCATATGACACCGAGATCATTGC  
CACGGTACGGAATTCGTCCAGAAGGAAATCTTCCCAATGCACCGGCCCTCGAACGTGGCAACAGCTACCCGCAAGA  
AATCGTCAATCGGCTGGGTGTTATTGGCTTGCTCGGTCGCCGGCTGCGAGGGTTTCTACACCACCGAGTTCATTCTCG  
GGCGTGCCGGCGCATTCGAACCTGGCGGTGCGCGCTG

:::Rv201T7.seq:::

GCACCGGCGTCTGCAATTGGTAGGCCTGCAGTTTGTGCATCAGGCCGATGCCGCGGCCCTCGTGGCCACGCATGTAC  
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CCAAACACATCGCCGGTCAAGCACTCCGAATGCACCCGGACCGACAGTCTTCACCGTCGGCGTTGGGCCCGGCGATC  
TCGCCGCGGACCAACGCGACATGTTCCACGTCTCGTAGATGCTGGTGTAGCCGATGGCGCGAAACTCCCCANGACAA  
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## Clone Rv204

:::Rv204SP6.seq:::

TGGTCCGTGTGCGCATACCAATACACGCGCCGGGCAACCAATCGGTGGCCATCGCCATC  
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CCGGTCAAC

## Clone Rv205

:::Rv205SP6.seq:::

GGCGTGTGGCCACCGGGGCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCGCC  
GACTTTCGCGGTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAACCTAC  
TTCATCCTGACGCCGGAACAAATTGACGCGAGCGGTTCCGCTGACCAATACGGTCCGTCCCACGATGACCCAGTACTAC  
ATCATTCGACGCGGAGAACCTGCCGCTGCTAAAGCCACTGGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCT  
GGTTCAAACCAAACTTGAAGGTGATTGTTTACCTGGGCTACGGCGACCCGGCCTATGGTTATTGCACTCCCCGCCCAA

:::Rv205T7.seq:::

CGTCCGTGNCCTCAANCGCGTGNNGCCGAAGCGGCTGGTTACGACTCCCTGTTTGTGATGGACACTTCTACCAACT  
GCCCATGTTGGGGACGCCCCGACCAGCCGATGCTGGAGGCCTACACGGCCCTTGGTGCGCTGGCCACGGCGACCGANCG  
GCTGCAACTGGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCCGACCTGCTGGCAAAGATCATCACCACGCTCGA  
CGTGGTTAGCGCCGGTCGAGCGATCCTCGGCATTGGAGCCGGTTGGTTTGAGCTGGAAACACCGCCAGCTCGGCTTCG  
AGTTCGGCACTTTCAGTGACCGGTTCAACCGGCTCGAAGAGGCGCTACAGATCCTCCAGCCAATGGTCAAGGGTGAGC  
GCCAACGTTTTTCGGCGATTGGTACACCACCGAATC

## Clone Rv207

:::Rv207SP6.seq:::

CCGCTTCCGTGTAACCGAGCANNGCGAGCGANCTGGCGAGGAAGCAAAGAAGAACTGTTCTGTGATAGCTCTTACG  
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AAACTGTGATAATCAACCCTCATCAATGATGACGAATACTCCCCGATATCAGGTCACATGACGAAGGGAAAGAGAAG  
GAAATCAACTGTGACAACTGCCCTCAAATTTGGCTTCTTAAAAATTACAGTTCAAAAAGTATGAGAAAATCCATGC  
AGGCTGAAGGAAACAGCAAACTGTGACAAATTACCCTCAGTAGGTGAGAACAATGTGACGAACCNCCCTCAAATCT  
GTGACAGATAACCCCTCAGACTATCCTGTGTCATGGAAGTGATATCGCGGAAGGAAAATACGATNTGAGTCGTCTGGC  
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## Clone Rv209

:::Rv209SP6.seq:::

TGACACCCAACAGAGGGCACTTAAGATGGCAATGCGGCCGCTACCTGCACGTTTTCGCGATGTCAGAGGATGCCGAG  
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AGGCCCGANTCNAGGCCGAAGCATATAGCGCGGCCGACCGCATTTCTGTCGACCGCAAGCGCGACCTCAGCCGACG  
CGGTGGAGCTACTGCTGCGCGCCATCACGCC

:::Rv209T7.seq:::

ACGGGCGACGCTGAGGTGGGCCGCGCTATTTCATGCTGTGCTCCACGTCCAGCGACGCACTGCGCCAGACGGCCCGC  
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GCGCACCGGCCGGTGCACACCGCGGTGTTGCCGCAACCTGCCGGAGCTCGTCGAGGGTTTGCGCGAGGTGGCCGAC

GGTGACCCCTCTATGACGCGGCGGTGGGACACTGTGATCTAAGACCGGTCTGGGTCTTCTCCGGGCAAGGGTCTCAGT  
GGGCGGCGATGGGCACCCAATTGCTCGCCAGCGAACCAGTGTTTCGCGGCCACCATCG

## Clone Rv20

::::::::::::Rv20SP6.seq::::::::::::  
ATACTCAAGCTTCGCGAGATCCGGATGGCACTCACGCTGGACAAGACCTTCACAAAATCTGAAATCCTGACCCGATAC  
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GACCTGAATTGGCAGCAAGCGGCGCTGCTGGCCGGCATGGTGCAATCGACCAGCACGCTCAACCCGTACACCAACCCC  
GACGGCGCGCTGGCCCCGGCGGAACGTGGTCCTCGACACCATGATCNAAAACCTCCCGGGGAGGCGGAGGCGTTGCGTG  
CCGCCCAGGGCGAACCCTGGGGGTTCTGCCGAGCCCAATGATTGCCGCGCGGTGCATCGCGGGCGGCGACCGCCA  
TTCTTCTGCGAATACGTCCAGGAGTACTGTCTCGGGG

::::::::::::Rv20T7.seq::::::::::::  
AGCTTATGTGGCCGCCACCTACCTTATCTAGCCTAGCTAACTAAATCCAGTGCCGACAGTGCGCGGCTGGCCACCCA  
GCATGAGGTTATGACCACGGCATATGCCAGCGCGTGGCGGCGATGCCGACGCTGACCGAGTTGGCCGCTAATCACAC  
CAGCCATGCGGTGTTGCTGGGAACGAATTTCTTTGGAATCAATACGATCCCGATCGCGCTCAATGAGGCCGACTATGC  
GCGGATGTGGATTAGGCGGCCACACGATGAGTATCTATGAGGGCACCTCCGATGCGGCGCTGGCGTCNGCACCGCA  
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## Clone Rv214

::::::::::::Rv214SP6.seq::::::::::::  
ATACTCAAGCTTGCCACCCATGCCGAGCAAGGTCGACTCAGCGATGACGAATTGTTCTTCTTCGCGGTGTTGCTGCTG  
GTTGCGGGCTATGAGAGCACTGCTCATATGATTAGCACNTTGTTCCTGACGCTGGCCGACTATCCAGATCAGCTGACA  
CTCCTTGCGCAGCAACCAGACCTGATCCCGTCGGCGATCGAGGAGCACCTCCGCTTTATATCGCAATCCAAACATCT  
GCCGCAACGCGCGTCGACTATTGCTCGGTCAAGCGGTCATCCGGGA

::::::::::::Rv214T7.seq::::::::::::  
CCGGGGTAGAACGATGCGATCTGGGCCATGTCGACATCGGTGGTACAGGTAAACCGCGCCGTGTGCGCGGTCTCGGAG  
ATCAGAACGTGGTCGAGTTGACACCGCGGGCTTTCAGCCAGTCGCGATAATCGGCGAAGTCGGCGCCTGCCGCCCA  
ACTAGCGGACCTCGCCACCTAGCACACCGATGGCGAAGGCCATGTTTCGGGCCACGCCCGCGGTGCATCATCAAC  
TC

## Clone Rv215

::::::::::::Rv215SP6.seq::::::::::::  
ATACTCAAGCTTGGCGGCAACGCCACTACCGGGCTCACCAGGTCCTGTGCCGCCACCGCCGGCGCCGAAAGCACCATC  
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TTGCACCCGGGATATTCGCGGTGGCGATCCCAACGAGGGTGTCAAGTCAGCGGTGTATCTGAGATGTCTCTACTA  
TCATCCGTTTGGCACCCGAGCGGGCATGCCCGCGGGGGTCAAC

::::::::::::Rv215T7.seq::::::::::::  
GTCGACGGCATCAAGGTCCGAGTGATGGTGTTCATCTCACCCAGGAAGGCGTGAAGTGGCTGATACCGTGGCTTGAG  
GATTCGGTGCGGGTCGCCAGTTAATCCGCCGTGTGCTCCGGATGAGCGCGACGGTAACCTGGAATTGTGCTGTGTGC  
TGGCTGTGTCGTTGTGATGAGCCTGTCTAAGTGGTGCCTAACCGTTTGACGAGCCGCGGCCCTCGCTGCAAACATTGAA  
GCCCGCACGTCTGGGTTTGTATTTACACAACGAGGGCGCTCCCGATCTGGCGCGCGCAACGAGGTGCNCACTATCCA  
TTCGAGGTGAACTGGACTCCTTGATGCTCATGCCGCTGCGGTTTTGTCT

## Clone Rv217

::::::::::::Rv217SP6.seq::::::::::::  
ATACTCAAGCTTGCGTTCGATGAAGTAGTCGTGGTCAGCGCCGCTCTTCGAGCTCCTTGGCGATGCCAGCAAGGA  
GTATCGCGCCGCGGACTTGGCCAGGATCTTGTGGCCTGTTCTTGACGATGCGGGCCCGCGGATCGTAGTTCTTGTA  
GACACGATGACCGAAACCCATCAATTTGACCCCGGCTCGCGGTTCTTGACCTTGCGTTACAACTCGCTGACGTCGT  
CGCCGCTGTCGGAATGCCCTC

::::::::::::Rv217T7.seq::::::::::::  
NGTCAAGCCGAGCATGCGCGAGGNAACGACGAACCAACAAGCCATGGTGGTTGGCGCCGTGAGAGGTGCGCGGTGCG  
CCACAACGGGAAGATCGCCTTGAGCGTCGCTCGACCGCCGCTCGAGTTGGGTCATAACGAAGTAGCTGATGCCGATC  
ATGTCGACGTTTCCGTCGATCAGCGTGCAGCGCGACCCACTCGACGAGGTCTCGGTGCCGCCGCGGCCAGGGCACC  
AGCAGTGACGATTCCAGGCGCCGTGCGG

## Clone Rv218

.....Rv218SP6.seq:.....  
CGATAATCGCTTCCGGTAAGTGCAGCAGCTTTACGACGGCGACTCCCATCGGCAATTTCTATGACACCGAGATACTCTT  
CGACCGAACGCCGGTGTCTGTTGACCAGTCAGTAGAAAAGAAGGGATGAGATCTCCCCGTGCGTCCTCAGTAAGCAGC  
TCCTGGTGCAGTTTATTACCTGACCATACCCGAGAGGTCTTCTCAACACTATCACCCCGGAGCACTTCTAGAGTAAAC  
TTCCCATCCCGACCACATATAGGCTAAGGTAATGGGCATTACCGCGAGCCATTACTCCTACGCGCGCAATTAACGAAT  
CCACCATCGGGGCCGCTGGTGTCTN

## Clone Rv219

.....Rv219SP6.seq:.....  
NAATACTCAAGCTTTCTCGTGATTACCACCCGTGTAATTTGGGATGGGCAAAAAGGCGAATCACCGCGTGGCCACAAA  
CGCCGGGAGGGACAATCTCGGGCGGCTAGGGCTTCTCGCGGGAAGGCCCGAACGTACGGCGTTTCAACACGTGCGCTC  
GCCCTCCGACCGCGAACATTCTGGGGATGGCAGCAACCTGGTATCACCTGGCCGGGCAATGATCTGCAGCGTCGCCGC  
GGGTAGTGNCCGCCCCGGGCGGCTAC

.....Rv219T7.seq:.....  
CCAAGTAGAGCATCGGGACATACGGAGTCAACTACCCGGCCAACGGTGATTCTTGGCCGCCGCTGACGGCGCGAACG  
ACGCCAGCGACCACATTACGAGATGGCCAGCGCGTGCCGGGCCACGATGTTGGTGCTCGGCGGCTACTCCAGGGTG  
CGGCCGTGATCGACATCGTCACCGCCGCACCACTGCCGGTCTCGGGTTACGCGAGCCGTTGCCGCCCGCAGCGGACG  
ATCACATCGCCGCGATCGCCCTGTTCCGGAATCCCTCGGGGCCGCGCTGGCGGGCTGATGATCGCCCTGACCCCTCAA  
TTCGGGTCCAAGA

## Clone Rv21

.....Rv21SP6.seq:.....  
ATACTCAAGCTTGCTGCAGCTTCTGTGACTGCTCCCGAAACCTGGGGGTGTGCCTGCTGTGTATGCACGGCATAACGG  
ACATCCTTCCCCTGAGACCCGCGGTCTGAACAGCCACGTGTCCATCATCAGGGGTCAACCCCGGCCAAGGGCGACGGC  
ACGCCAAGTTCCGCCGACCGTTAACCTAGTGCTGTTAGCTTCATTTGCTGCGAGCAAAACAGCTGGTCCGCCGTTAGGA  
ACTGAATTGAAACTCAACCGATTTGGTGCCGCCCGTAAGTGTCCTGGCTGCCGGTGCGCTGGTGTT

.....Rv21T7.seq:.....  
AGCTTGCAGCGGCTGGCGATCGCGGTTCAAGGCGCGCTCTTCGAGCACAACGAGCGAAGACAGCTCGGCGACGGAGCC  
TTTATCGACATCCGTTCCGGGCTGGCTGACCGGCGGCGAAGAAGTCTGGACGCGTTGTTGTCGACGGTGCCGTGGCGA  
GCCGAGCGCGCTCAGATGTACGACCGGGTGGTCTGATGTGCCGCGGCTGGTGAGTTTTACGACCTGACCATCGAAGAT  
CCGCCGCATCCGACGCTGGCGCGGATGCGCC

## Clone Rv220

.....Rv220SP6.seq:.....  
AATACTCAAGCTTGCGCAGCAGCAGGACGTCGAGTGGCGCTTGCACTGACTTGGCGACCTCAAAGGCCACCGGTACCC  
CGCCGCGCGGCAAGCCAAGGACNACNACGGCCTTGCCGGATAGCTGCGCCAGGCGTTGCGCCAACCTGGCGTCCAGCGT  
CGCCACGATCGTCAAAGAGCTTCATCTGCCGAGTGTGTGCCATCTCATGGCTCCAAATATGGAATTAGGTCCCTGGG  
CCGACTGACGACAGTCCCTCAGCGACCGGATTGCGCATCCCGCCTTGACGCTGCTCCGCAATCCCGGGCTTGCGTC  
CGCGGAAGCGAACTCGGCGGCGCTACGGTGGTGGCTCACTTCGGCCGTGC

.....Rv220T7.seq:.....  
GGTTGGTGCGGTCCACCTTCGCGGCGGCGGCGGATATGCCTTGCTGGTCTTGCTCATTGATATCCAATCTATGGGT  
CGTGGTTACTCAGCGGGCCGAAGCTGGCCCTCCACGGGTAGGGCCCTATTTCGACGGTGATGCCATCGACCGAGCGG  
TACCGGCGATGATCTTGGCCGACGCTGACGCTGCTTGGCGTTGAGGTCCGTCTTCTTGGTCTCGGCGATTTTCGCGGA  
CTTGATCCCAGGTGACTTTGGCGACCTTGGTCTTGTGCGGCTCCGCCGAACCTTCGCCACACCGAGCGGCTTAAGCA  
GCAGCTTGGCGGCGGCGGCGTCTTCAGCGTGAAAGTGAAGCTACGGTCTTCATAAACGGTGATCTCACCGGGATGA  
CGTTGCCGCGCTGGTCTCCGTCGCGGCTTGACGCCTTGACAGAACTCCATGATGTTGACCCGTGCTGACCGAACGC  
GGGGCCCACTGGCGGGG

## Clone Rv221

.....Rv221SP6.seq:.....  
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CGCCGCGCTAGGCCCAATTGCCCGGCTCCTCCTCGGGCCGTTCCACAACCCGCATCGTCGCCGGGCTAGGTTCAAGCC  
ATGCCGGTAAACCCAGGACGCCAGTGCTGATCGGCTATGGACAGGTCAACCACCGAGGCGACATCGACGCCNAAAAAT

CAGTCCATCGAACCCGTCGACCTGATGGCCNCCGCGGCCCGGAAAGCCGCCGAGTCCACCGTGCTCGAAGCGGTGGAT  
TCCATCCGTGTGGTGCACATGCTGTGCGCGCATTACCGGAATTCCTCGGC

.....Rv221T7.seq:.....  
NCCTGGTTTCATGAAGTGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCGGCGGTGGG  
TGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCTGAAACCAGCTTCCATATCCCGCGACGAACGACGCC  
AGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCTTCTCCACCGACCGGGGCGGGTGTGGGGTG  
TTCGGCAACGGCAACCAAGTTGGTCCACACTGCCGACGGGCGCCGCAATCCGTTACCGAACCAGGCCGCCNAAACA  
ATTCCGCCCGATCCCATAT

#### Clone Rv222

.....Rv222SP6.seq:.....  
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CACGGACGCCCCATATATGTTCCGGGTGGGCAAGAACGGTCCCTACCTGGAACGTTTGGTGGCCGGCGACACCGGTGAG  
CCCACGCCGCGAGCGGGCAACCTCAGCGACTCGATTACCCCGGACGAACTGACTCTACAGGTGGCCGAAGAGCTCTTT  
GCCACACCGCAACAGGGACGGACTTTGGGCTTGGACCCAGAAACCGGCCACGAAATCTTTGCCAGGGGAAGGCCGTT  
TGGGCCTTATGTTACCTATATCCTGCCGGAACCTGCGGCTGATGCGGCCGCGGCCGCTCAGGGAN

.....Rv222T7.seq:.....  
AGCAGCTAGCCGCGCTCGCCGCGCTGGTGGTGGTGCATGCTCGCAGCCGGATGCACCAACGTGGTGCACGGGACCG  
CCGTGGCTGCCGACAAATCCGGACCACTGCATCAGGATCCGATACCGGTTTCAGCGCTTGAAGGGCTGCTTCTCGACT  
TGAGCCAGATCAATGCCGCGCTGGGTGCGACATCGATGAAGGTGTGGTTCAACGCCAAGGCAATGTGGGACTGGAGCA  
AGAGCGTGGCCGACAAGAATTGCCTGGGCTATCGACGGTCCAGCACAGGAAAAGGTCTATGCCGGCACCGGGTGGACC  
GCTATGCGCGGCCAACGGCTGGATGACAGCATCGATGACTCCAAGAAACGCGACCACTACGCCATTCAAGCGGTGCTC  
GGCTTCCCGACCGCACATGATGCCGAAGAATTCTACAGCTCCTCCG

#### Clone Rv223

.....Rv223IS1081N1400.seq:.....  
CGCGACTGGCTCCCCGGNCGGCTGCTCGGGTCCGCCGATAGAGACCGGGATGTCGCCCCGACGACGGGCAGCCGGGTTG  
CGTGGGACGGGGCGGGGTGCGGCAGCCCAAGCAACGGGCTAGTCCCCGAATCCTACGGAGCCGTCACCTACGCCTAC  
GTAATAGTAGCTATCAATAACAGTTGACATACGCAACGATCTGTGAGATCAATATTGCCTGACGCATGTCAAGACAGG  
CGTCAAGACAGGTGTCAATAATTGCTCCGCTGGTGACGGTAACGGTCTGTCGGGTGTGTGACGCCTAAGGAAGGAG  
TGTGGGTGGTGACGCTGAGAGTGTTTCTGAGGGTTTGGCGGCCGCCAGTGCGGCGGTGGAGGCGTTGACCGCACGGC  
TGGCCGCCGACACGCTGGCGCGGCGCGGCGATTACGGCGGTGGTGGCGCCCGGGCGGATCCGGTGTGCTTGCAGA  
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.....Rv223SP6.seq:.....  
ATACTCAAGCTTATTGAACCGCGGGTCGAGGCAAGTGGACCTCATAACGACTCGGGTCCAGCGACCGCGCCAACAC  
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CTCACACCGACCGCTAGTTGCGGATCAGAAATCCGTTGGGCGCGGAAGTCCAGCCGAATTTGTTCTCCCGCTCCGCAT  
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.....Rv223T7.seq:.....  
GTCTCGATCATGGCCAAAAGAGCTCGACGAAGCCGTAGAGGCGTTTCGGACCCGCCGCTCGATGCCGGCCCGTATACC  
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GGCGTCAACGCCGAGGGCTACCGAGAGATCCTGGGCATCCAGGTACCTCCGCCGAGGACGGGGCCGGTGGCTGGCG  
TTCTTCCGCGACCTGGTGCCTCGCGGCTGTCCGGGGTTCGCGCTGGTACCAGGCGACGCCACGCCGGCTGGTGGCC  
GCGATCGGCGCCACCTGCCCGCAGCGGCTGGCAGCGCTGCAGAACCCACTACGCAGCCAATCTGATGGCAGCCACC  
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AATATGATCGGGTTCTCGAC

#### Clone Rv224

.....Rv224SP6.seq:.....  
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CCACGAGGTTGGTGCTCGGCGGCTACTCCCAGGGTGCGGCCGTGATCAAGATCTTCACCGCCGCACCACTGCCCCGCC  
TCGGGTTACGCATCCGTTTGGCCGCCGCC

::::::::::Rv224T7.seq::::::::::

GCCCCGTGTAATTTGGGATGGGCAAAAAGCGAAGCACCGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGGCT  
AGGGCTTCTCGCGGGAAGGCCGAACGTACGGCGTTTCAACACGTGCGCTCGCCCTCCGACCGCGAACATTGCGGGAT  
GGCAGCAACCTGGTAGCACCTGGCCGGGCGATGATCTGCAGCGTCGCCCGGGGTAGTCTCCGCCCCGGGCCG

Clone Rv225

::::::::::Rv225SP6.seq::::::::::

ATACTCAAGCTTCTTTGACCGAACGCGTCCACCGCACCGTGAGATTGGTGGCGCCATTTCGTGCTGGTGTAGCTGCTG  
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CCCAGCTCGACCGCGAATTACGGCGGCCGCAACGGCCGCCGGAAGGCGTCACGCAATCGCTTATCCTTTCCAGGTTCC  
CAATCCTCCGCTTACTTGGGTCCTTCATCGG

::::::::::Rv225T7.seq::::::::::

GGCAGCGGCGACAACCGGAACGTCCGCACGGTGCTCAATCACGGGTGCACGGTGTGCATCAGAATGGCGGGGGTTTCGT  
TGTCGCGGTGAGGCGTTCGGCGAGGAGGTAGTGTCTACCCCTTGCCCCGCGGTTTCGTGCGGACTGAAAGGGATTTTCAT  
TGGGAACCCACGGCTGCGTATCGCAGGGCCTCGGTGACGTCTGCTTCTCNAGCTCAGGAAGTTCGGCGAGAATCTCG  
GTGGATGTTATTTGGTCCGCCTAC

Clone Rv226

::::::::::Rv226SP6.seq::::::::::

ATACTCAAGCTTCTCGGCTTCTCTGATAGCCTGAGAAGAAACCCCAAGTTAATCCGCTGCTTCACCTATTCTCCAGC  
GCCGGGTTATTTTCTCGCTTCCGGGCTGTTCATCATTAACTGTGCAATGGCGATAGCCTTCGTTCATTTTCATGACCAG  
CGTTTATGCACTGGTTAAGTGTTCATGAGTTTCATTCTGAACATCCTTTATTTCATTGTTTTCGCTT

Clone Rv227

::::::::::Rv227SP6.seq::::::::::

ATACTCAAGCTTGGTGACCGGCACCGCGATACGTTGCGGCAGGCATCTGGGCTGGCGGTGGTTCGCCGCTCCGAAGCC  
GTCGAACACCATCGCCAGCGCGGCTTCCACATCAACGACCATTTTCGGCCAGCTTGC GGCGCATCAGCGGCTTGTTCGAT  
GAGCGCCCCACCGAATGCCGCCGCTGCCCCGGCGTATCACATCGATTTCGACCATCGCGCGGCGCGGCTGCGGAGGGC  
GAACGAGGCGGTGCCAACCGCAATCTGTTTGGTCAGCTCCCTCATGCGGGTTGATTCTTGCCGTCGGGACGGGCC  
GCGTCATGCGCTCGGTTTCGCC

::::::::::Rv227T7.seq::::::::::

CCGTTGCGCAGCGTGAGCCGATAGTTGACATCCGGCTCGGTGAAGGTGAAATCGATGGCCAGGTCGAGGTCCCATGCG  
CGTGGGCCATTGATGCTGATCGCCAGGACGTCAAAGATTTGGTCCGGCGTCAGCTGGGCGAAAAACGTGGGCGCCGGG  
ACTTGCCCCGAGCTGCCCGGGTTCCCGTCGCGCAGCTCGGCGGCCCCGGTCAGAAAGAAATTGCGCCAGGTCGCACAC  
TCCGCGCCGTAGGCCAGCTGCTCCAGGGTGTGCGCATAGAGCCCCGCGGCGCAGCGTGCTCGCTGTTCGGCGAACACC  
GCATGGTCGAGAAGCGTTGCCGCCAACGGGAAATCACCTGCGTCGAAAGCTTCGCGGGCCAGCTCCAGCACTCGGTC  
GATGCCACCCAACGCGT

Clone Rv228

::::::::::Rv228SP6.seq::::::::::

ATACTCAAGCTTTCGGATGTTACCCCTGACAGCGTGAACCTATGTCNAAACACACGGCACCGGAACGGTGTGGGGGAC  
CCCATCGAGTTCGAGTCGCTGGCGGCCACTTATGGCTGGGTAAAGGCCAGGGCGAGAGCCCGTGC GCATTGGGGTCG  
GTCAAAACCAACATCGGCCACCTGGAGGCGGCCCGCGGTGTGGCTGGATTTCATCAAGGCGGTGCTGGCGGTGCAACGT  
GGGCACATTCCCCGCAACTTGCACTTCACCCGGTGGAACCCGGCCATCAACACGTGCGCGACGCGGCTGTTTCGTGCCG  
ACCGAAAGCGCCCCGTGGCCGGCGGCTGCCGGTCCACGCAGGGCTGCGGTGTCATCGTTTCGGCCTCAGCGGGACCAA

::::::::::Rv228T7.seq::::::::::

CCGGTAACAGATCAGCTCGTCGACCTACTGCCGGGGTGAATTCCCCACCGGTGCTGCGCGCTGCCAGTAGTGCA  
CCTTCTTGACGCCTCGAAAAGGGGAGTCGGTCGGGTAGGTACCGTCAGGAGCCGCTACCCAGGTTGGCGCGGTGAC  
CGGTCTCTCGAGTATCTCCCGCACCGCCCCACCGGTGCGGTCTCGCCCGGATCCACTTTGCCCTTGGGCAGCGACC  
AGTCGTCGTAACGGGGGCGGTGAATGACAGCGATCTCGACCGGCCCTTCGGAATCGGCACTGCCGGGTGCGCAGAAC  
CCGCACCGGCGGCGTACACAATCCGGCCCGCGAGCGCCGGCGGGCGGACGANTTCTGGATCGACACCTCAACTCCTG  
CAGGTCAATTTCGGCCAAGCTGCTCGCGGTGCTGGATGTGGT

## Clone Rv229

:::Rv229SP6.seq:::

ATACTCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCACCCACCGCGCGGGTCGGGCGCCGGGCCCCGG  
GCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCCCGGCTGCGCTACGTCGAGCCATACCGGGCG  
GAGCTACATCGGCTCGGCCGCCAGTGTTCCGGGCCCTCTTTCGAGGTCGAGGTCATACCGATTTGCGCATCCGCAGC  
CGCACCTGGTCTCTGTACCGTGCCCTACCTCTGCTTGTGCGGCGGGGCCA

:::Rv229T7.seq:::

TCCGTACGGCCCGGGTACGCTTCGGTCGCAAGTGTGCGAGTGATAGATGACGACCGGGACCTCGTCGGCATCTTCCATA  
GCCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGGTAGAAGGTCGGCGAGCGCTCGGCATTGGTTCATCGGGATA  
TGCCGCTCGGGACGGTCAGAGCCCTCGGTCGCGCCAGCACTCCGCAGGCTTCGTGCGGGTGGTTCGCGACGCGCATGG  
GCCACCATCCATCCACAGGTCTGCGCAATCACCCG

## Clone Rv22

:::Rv22SP6.seq:::

GGACACATTGCGAACATTGATGACAAAATAGAAATCATTGATGGTTTGAAGTCACCGAGCCGATCAAGCCTTCGCCGAG  
CCAAATTCGAATCAAGAGGCCCAAGCCCGTACCAATCAGCCCGCAACGAGGGATTCCGTCATTATCAGCCAAAATAA  
CTGCTCTCGGGTTACACCCAAACAGCGCAATATGGCGAAAAACGGTCGCCGTTGCACGACATTAAATGTCACGGTATT  
GTAAATTAAGATAACCCACCAACAAGGCAATCAAATGAGAGCGGTTAAATTGACCGTAAAAGCGTCCGTCATCTG  
TTTGACGGTGTCCCGTTGGGTNTCCGACGTTTCCATACGCACACCGGCCCGGCAGTCTTTGTTGGATGCGTGTTCAGT  
GGCCTCATCTTTGATGATCA

:::Rv22T7.seq:::

GCCTGGCCCAGGTGAAGGCCGACCTCGACGCCAAAGCCGCTGATCCGGCACATGAGTCGGTGGACTGGGACTTGAAGT  
CGCTGCGATGGGCGTGGAACCGAGCCAAAGATGACGTGGCGCCGTGGTGGGCCGAGAATTCCAAGGAGTGCTACTCGT  
CGGGGTTGGCCGATCTGGCCAGGGCCTGGCTAATTGGAAAGCTGGCAAGAACGGGACCCGCAAGGCCGGCGGGTGG  
GCTTCCCGCGATTCAAATCCGGGCGGCGTGATCCTGGCAGGGTGCGGTTTACCACCGGCACCATGCGCATAGAGGATG  
ACCGGCGCACGATCACGGTCCCGGTGATCGGGCCGCTGCGGGCCAAGGAGAACACCCGCCGGGTGCAACGCCACCTCG  
TGAGCGGGCGCGCGCAGATCCTGAACATGACCTTGTGCGAGCGTGGG

## Clone Rv230

:::Rv230SP6.seq:::

TAACTCAAGCTTCAAGTCCGCNGTCCGACCCTGTTGACGGCTACCTGAATCAACCCGATGCCCCGCCGCGGGCTTCG  
ACCCGACAGCTGGTACCGCACCGGCGACGTCGCGGTGGTTCGACGGCAGTGGGATGCACCGCATCGTGGGACGCGAGTC  
GGTCGACTTGATCAAGTCGGGTGGATACCGGGTCGGCGCCGGTGAAATTGAAACGGTGCTGCTCGGGCATCCGGACGT  
GGCGGANGCGGCAGTCGTGCGGGTGCTCGACTATTATCTAGGCCAGCGGATCGTTGCCTACGTAGTCGGCTCAGCGAA  
TGTCGATGCGGACGGGCTTATCAACTTTGTTGCCCAACAACCTT

:::Rv230T7.seq:::

CCATGTCGCCCCAATATCGTCGATGTTTCGCGTCGTCCGCCCTCGCGCACGTGGTCTGTACCAGTCAACGTTAACGCC  
GCCGCACATGTCTGCGGCCGGGCAAAACGTGAAAACGAGCGGGCGACTGCAATGTCATGACACCGACGCCGCCGA  
TGGGCCCAGGGTCTGGCAGATTGATCTGTGCGGCCAGTGCCAGCAGCGTCGCCCTCGTCATACGGCCGGCCGACGAGT  
TGAAACGACATGGGCATGCCGTGCGCGTCGAAGTCCCACGGCACACGGCCGCGGGCTGGCCGGTCAGATTCCANACT  
TGAAAGTACTGAAGCCGCTGCACACACG

## Clone Rv231

:::Rv231SP6.seq:::

CGAAAGCGTGAAACAGCTCGCGGCAGCCCCGACGTGCTGCGTCGGATAGCCGGCGGGCGAAGATCAATTCCAGGCAG  
CTCCCCGACAATGCGGCTCTGCTGGCCCCGCAACGAAGGACTCGAGGTCACCCCGGTGCCCCGGGGTCGTGGTGACCTG  
CCGATCGCACAGGTTGGCCCCACAACCGGCCGCTTGATGCCCGGTGCGCAAGCCCGGCAGTTGCCAAACCCAGCGTGAT  
CNTGCTCNGCTCTNTANTTCGGCGAAGAAGTGGCTCGCCTGATCACCTACCATCGGCCAGGATCTGCGTGTTCATCACA  
ACGCTCGCCAAGGAGGTTGTTGTG

:::Rv231T7.seq:::

TCCGCCACGCTTCGCGCCGCCCGGCATACGGCGCGTACCGATCTCCGCGTCATACACCGCGGGTAATCGCCGACGGTG  
CCGGTTCGCGAGCCGAAGGTGACGACGCTGATTGAATCGAGTTCAGGTCCAGCGGGTGGCGCAGCAACGGCGCGAGC  
TCAACGACGTCAATCACGTTGTGCTTTCTACGGTACCGACCCGGTGACCGTAGTCGCCCCGTGCGCTCGGCCGAGA  
AGCTGCACCGCCACACCGCGACACCGTCTTGACGCGGGACCCACCCCGGATCGGTTGTTGGCCAAGGTAATTGGGTC  
ATTCCATTGACGGGACGCCGACCC

## Clone Rv232

.....Rv232SP6.seq:.....  
CATTCTTTAACAGTTGTTTTGGGCTCGGCATGGTTAGCCAACGTTCTGCGGTCCACCATATCATCTTGGTCCGGTAGC  
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GGCCGNCGCGGTCCCATCACAACCTGAACCCCCAACAGGGACATGCTTATCGGTAGGGCGCGGCCAAGGCGGCAGCA  
ATCGCATCACTGCGCTCTGCGCGTCACTATTAAACCCACCCGGACTTCACTTCCACCACCCGAATGGCGCCCGGTCTAT  
TGATCATCTGGCGCACCGCGGATAA

.....Rv232T7.seq:.....  
CGGTGTCCTGCAGTTGGTAGGCCGTCAGTTTGTGCATCATGCCGATGCCGCGGCCTCGTGGCCACGCATGTACAGCAC  
CACGCCGCGCCCCCTACGGGCGAACATCGCCAGCGCGGCGTCCAGCTGAAGCCCGCAATCGCAGCGGCGTGACCAAAC  
ACATCGCCGGTCAAGCACTCCGAATGCACCGGACCAGCACGTCGTACCGTGGCGTTGGGCCCGCGCATCTCGCCGC  
GGACCATGCGCGACATGTTCCACGTCCTCGTANATGCTGGTGTAGCCGATGGCGCGAACTCCCCATGACGAGTCGGA  
ATCCGCGCCTCGGCGACCCGCTCAATGTGCT

## Clone Rv233

.....Rv233SP6.seq:.....  
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CATTACCTCACCGATGGTGCGCTTGTGCAGGCCGCCGGGATACCCCGAGTGCCGGTAAACCATCTTGTGCTGCAGTTT  
GTCGCCGCTGATGGCGACCTTGTGCGCGTTGATCAGCATNACNAATCACCGCCANCGACATTGGGGGCGAACGTCGGC  
TCGTGCTTGCCGCGCAGCAGGCTGGCCGCCGCGACGCAAGGCGCAACCACACGTCCTGGCGTCGATGACGTACCA  
CCATCGCGTGGTGTACCCGCCTTGGGC

.....Rv233T7.seq:.....  
GCGGCAAAATGAAGCACTCNTGGCCACTNCCGCCGGGAGGACAATCTCGGGCGGCTAGGGCTTCTCGCGGGAAGG  
CCCGAACGTAAGCTTTCAACACGTCGCGTCGCCCTCCGACCGCGAACATTCTGGGATGGCAGCAACCTGTTAGCAC  
CCTGGCCGGGCGATGATCTGCAGCGTCGCCGCGGGTAGTCGCCCCCGGGCGGCTACAGTCTGAAACGCGATGACCATC  
GATGTGTGGACGCCGATCCGACNCAACGGTTCCTACACTGTGATATGTTGCGCTCGCTGCGCCGGTGGACGGTGGGT  
CTATCCCGGA

## Clone Rv234

.....Rv234SP6.seq:.....  
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CGGGGTGATGCCCGCGAGCAGGATTGGCGAGCGGNCGGTCAGCCGGGTGAACCTTCGTCAAGAGCTGACGCTGCGGTTG  
GGGAGGCGAATCATGGTTCGGTGCCTAGCCTCGACTAGGCCCGG

.....Rv234T7.seq:.....  
TGACAACGCGGCGGCGATTACCCCGCTACCGCAGCAGCATGACGCGGTAGCGAACACCGCCGGATGCAGCGCAGGTGC  
GTCGATGTGCTCACGGAATCGCCCCGGCACCGCGATCTCGAGGATCACCAGTGCCACCCCTGCAGCGCGACACCGAC  
GATTCCGTACACCGCCACGCGGATCAGGCCCTGGGCCAGCTGATTGGAGCTGGCGTATATGGCGGCGATGGTGACGAT  
GGTCATCGCCTCTTACATTTGTGGCGGCCAGAACACGGCGTTGGGGCGGCGGTGATGAACACTAGGCGACCANATCC  
CCGGGTCAACAGGTTGACCATCC

## Clone Rv235

.....Rv235SP6.seq:.....  
CGCGGACATCCCGAACGAGGACACGCGACCGCTTCGGTGTGTGATCTATCAGGGCTCGCACCACGCGCAACCGCTTCC  
GGCTACCTAGACGCGGT

.....Rv235T7.seq:.....  
GCATGCGGGTGATGCCGTTCTCAGTGCGCAACAGCGTTTCGACGCGGCATACCCAGCCGCACATGCCGTGCACGCCGNN  
GCCGGGGCGGGAAATCT

## Clone Rv237

.....Rv237SP6.seq:.....  
CTCAAGCTTCAGNCCNTCTAAGCGGTCTGCGCGGCGATCGCAAAGATCGCCCTTTGCCGGCGTTGGGGGCTTCTGCTC  
GGGGGTGTTGTACACCTTCTCGAACACCTCGGCACCGACACCACACCGTTCGGCTTGAACACCGCCAACATCGGCAGC

ANATCTTGATGTCCTGGTGAATCCACGGTGACTTTGGAGTGGAAGGCGGCCATACTGATCGCGCGCGCCACCACATGA  
GCTAGCGGCAGGAAAACCAGCAGCCGCTCACCTTGCGCAGCAGCGTCGGGTGATATGCCTGGCGCCC

::::::::::Rv237T7.seq::::::::::  
AGTCGAANGTCAGTCCGGTCTCCTCTCCGACTACGGCCAAGAACTGGGGCGACGGTGTCAGTGCAGAACAGCGGAAAC  
TGGTGGCGCCCTAGGCGAGCGAACGCTCACAAACGGCGGTGACCGCTTCTGGTGTGACCATCGAGCCGTGCCCAGC  
CCGGCCGCGTGCCGTGAGCCGATCCACTGGATGCCCTTCTCGGCGGTTTCAATCANGTACAGGCGACGTTTCCGACC  
ATCGTGCCGGGGCACGGTTAGCGAGAAACGCCGACTTCACCGATTGCCTCGGTGATGxxxxx

Clone Rv23

::::::::::Rv23T7.seq::::::::::  
AGCTTCGCGGCGTGGCGATCGCGGTTCAAGGCGCGCTCTTCGAGCACAAACGAGCGAAGACAGCTCGGCGACGGAGCCT  
TTATCGACATCCGTTTGGGCTGGCTGACCGGCGGCGAAGAACTGCTGGACGCGTTGTTGTGACGGTGCCGTGGCGAG  
CCGAGCGCCGTGAGATGTNCGACCGGGTGGTGTGATGTGCCGCGGCTGGTGAGTTTTCACGACCTGACCATCGAAGATC  
CGCCGATCCGCGAGCTGGCGCGGATGCGCCGGCGGCTCAACGACATCTACGGCGGCGAACTGGGTGAGCCCTTACCA  
CCGCGGGGCTGTGCTACTACCGCGACGGCTCTGACAGCGTCGCTGGCATGGCGACACCATTGGTCGCGGCAGCACTG  
AGGACACTATGGTGGCGATCGTCAGCCTCGGCGCCACCGCGTCTTCGCGCTGCGGCCGCGTGG

Clone Rv240

::::::::::Rv240SP6.seq::::::::::  
AGCTTCAGCTGATACTCGACAGCCCCACTCGGGCCAATACGTGAATGTCTAGCATCTTCACCCGTTACGGGCTANT  
CGAGTAGTAGACATTGATTAGCCTGAACGTACCTCCGACGCCAGCTGACGAACGGGTATGACGGATGGATTTCTGTGGT  
GTCGCGCCCGAGGTCAATTCTGTTACGGATGTATCTCGGGGCCGGATCGGGGCCGATGTTGGCGCCGCGGCGGCCTGG  
GACGGACTATCCGACGAACCTGGCGGTGGCGGCGCTCGTGGTTTGGGTGGTGACCTCGGGCCTGGCGGATGCGGCGTGG  
CGCGGCCCGCGCGGTTGCGATGGCNCGCGCGGT

::::::::::Rv240T7.seq::::::::::  
CTGGTCATGGACGTTGCTCCGGTAGTGGCTCACTGCCGATCCTCCTCGTTGAGAGTGCCACCTCAGGGTTGGGTAGGG  
TTGGGTACTCGAAACCAAGTTACCCACCAGTAACACCGTCAAAATATATCCGTTGCATAGGTCAATGCAAGTTGATGT  
GAGCTACATTGCAACCAACTAACCACCGGTTGGGTTAGCGGTGATCCTGGCCGTGTCGGTCTCTCACCTGCGG  
TGATAGCGATCAAATGAAGAATATGCGGAGTCTAGGGCGGACGCGCTGGCANCGTAGATCATCGGCTCACGCGGATG  
CGGCCTCTTGGTACGGACATGCGCGCG

Clone Rv241

::::::::::Rv241SP6.seq::::::::::  
CTCGTGAGTAGCACCCCTGTAATTTGGGATCGGCCAAAAAGGCGAATCACCGCGTGGCCACGACAGCCGGGAGGGACN  
ATCTCGGGCGGCTAGGGCTTCTCGCGGGAAGGCCCGAACGTACGGCGTTTCAACACGTGCGCTGCGCCCTCCGACCGCG  
AACATTGCGGGATGGCAGCAACCTGG

::::::::::Rv241T7.seq::::::::::  
GGATCAACTACCGGCCAACGGTGATTCTTGGGCGCCGCTGACGCGCGAACGACCCAGCGACACATTACGAGATGGCC  
AGCGCGTGCCGGGCCACGATGTTGGTGCTCGGCGGCTACTCCCATGGTGCGGCNCGTGATCGACATCGTCACCGCCGC  
ACCACTGCCGGCTCGGGTTACGCAGCCGTTGCCGCCCGCAGCGGACGATCACATC

Clone Rv243

::::::::::Rv243SP6.seq::::::::::  
AGGACCGTCAGCACGGCGACGTGCTACTCGCCGAGCAGTGGGAATCGCTCTGCAGCAAACATTACTCTGCGCGACGT  
TCGAGATGACCTTCTGAATGGACGGATCTACCTGCCGCGGACGACCTGGACCGCGTATGCGTCCGCCTCCGCCTGGA  
CGACACCGGGGCACTCTATGACCCCGACGGACGGCTCGCGGTACTGCTGCGGTTACCGCCGACGCGCGACGGTACG  
CGTCGGGACTGCGCTGAGTCCANCTCGACGCCGTAGCGCTGCTGCTGTGCGGCCATGTCTGGCATCTACCGCCGTCG  
CTCCCTTGA

::::::::::Rv243T7.seq::::::::::  
CGACTCTGTTGGCCACTGCGGGTCGATCTTGGCGCCGCCCGGTCGTGGAACGCCCCAGGTACCCGGCGGCGCACCGC  
GGTCAGCGCGTCTGTTGGCAGCGTGGTCACATGGAAGTGGTCGACGACGAGCTTGGCGTTGGGCGAGAGCCCGGGCGT  
GCGGATCGCCGAGGCGTATGACGCGGCGGGTTCGATGGCCACCGTACTGGATGCTCTCCCGGAAGTGGGTGTGCGCG  
CTTGACGCCATGCCAGCACCGCCGCGCGCGCGGCTTCATGCTGCCATAAACCTGATACCGGCCAGGTGACACNA  
ACCNGTATCCACGGTCAACCC

## Clone Rv244

.....Rv244SP6.seq:.....  
CACACGGACGGCGGTGCGGACGCAGCTGACGCGCATGGTGGTCAGCATCGCGGCCGGTCTGCTGTTGTATGCCTACTT  
CGCGCCGCGCAAATGCTGGTGGGCGGCGGTGGTGGCGCTCGCATGGCTGGGCTGGGTGCTGACCCAACCTCTCGAACCA  
CACCGGTGGGTGGGCTGGGCTATGGCCTGCCATATCGGCCTGCTGTTCTACN

.....Rv244T7.seq:.....  
CCGATATCCGAGCCGATAGCTGGCGGGCTCGGGTGGTNGCCAGCGGCGCTGCGACGAAAGTGTGACCGTCATGAAACA  
GACACCACCGGCGGCCGTGCGCCGTGCTCACCTGCTCGAGATCTCAGCATCCGCAGCCGGTGTGATCGCGCTTTCGGC  
GTGTAGTGGGTGCGCGCCCGAGCCCGGCAAACGCCGGCCGACACAACCCCGGAACAGGAAGTCCGGTCACCGCGCC

## Clone Rv245

.....Rv245SP6.seq:.....  
GCTTCAGGACAAATTGNATCCCTATGCACCCGTTGTACGCCGATGAGTGAAGACTGCACGCAATCGCCGGAATCCGG  
CAAAACCTTGACAAGCGAAATCAACCGGAGGCTGACAAGGCAACGTCGGTGATCCGTACCGCCTGGTTGGACAAACG  
GCAGAAAGGCGCCTCGTCCGGTCCATCTACGCCGAGCACACTGGTGATAGCGCCATCGGCATCGGTGCGGCCACGGTGG  
AGACGAACGTCCGCNNGCGTCTGGGTGAGTAACCCGCCGACCAGTTCTCGGGCAAGCTGGTCAACATCGGGCGCCACG  
TCTCCAAC

.....Rv245T7.seq:.....  
GTTTGGCGGCCTTATTGCACTGAGGTGCTCAATTGACCCACAGCGGAAATGCCGACTATTCGCAGGCCTCCTTCGCCT  
TGGTGCCGGAGATGGGCTCCGCGGGAACCGCATGCAGGTATATGACCTCGGTTTCTCGGGTGCTACCGCGTGCCTTG  
TCGAGGATGAACTCGGCGTTGGAATTGTCCAGCCGGCCCAATTCATCGAGCGCAGATTCTACACATGGCCGCGCGCG  
ACATACCTTACCGTGATCTGCTCCACACGGACCGCCCTGTCTGGGATCTGCTCACGGGTAAAGGAATTA

## Clone Rv246

.....Rv246SP6.seq:.....  
GCGCACTCCTCCTTATCGCTCCGCTCTGCATCGTCGCGGCGCGGTGAGGTGCAAACGCCTTCGGGGGTGGGGGTCTTG  
CGGAGCACACCGGATACGGAGCGCAACGCGTCCGCTTGTGCGGGCAAACAAGTGTGCAGGNNCCAATGCCATGTCCAG  
CAGCTTATCAGTGTCTGAACGTGCGAACGTGCGGCCTTCGCGGGTGCCTGAATCTCTACAAG

.....Rv246T7.seq:.....  
CGCTGAAAGCCACCATTCGCGGGTTCGGGCGCCGGGCTCGGGCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCG  
CGACACCACCGGCTGCGCTACGTGAGCCATACCGGGCGGAGCTACATCGGCTCGGCCGCTAGTGTTCGGGNCCTC  
TTTCGAGGTGAGGTCTGA

## Clone Rv247

.....Rv247SP6.seq:.....  
TGTAATTTGGGATGGGCAAAAAGCAAANCACCGCTGGCCACAAACGCGGGGAGGGACAATCTCGGGCGGCTAGGGCT  
TCTCGCGGAAGCCCGAAACGTACGGCGTTTCAACACGTGCGCTCGCCTCCGACGCGAAATTTCGG

.....Rv247T7.seq:.....  
CTTGGGCAACATGCTGAGGATCGCCTTTTACCACGCGGTGCGGGTGGCGTTGCATTAGCTCACCGATGGTGCCTTG  
TTGCAGGCCCGCGGATAACCGAGTGCCGGTAAACCATCTTGTGCTGAGTTTGTCCCGCTGATGGCGACCTTGTGCG  
GTTGATCACGATGACGAAGTCACCGCCATCGACATTGGGGGCGAACTCGGCTTGTGCTTG

## Clone Rv249

.....Rv249SP6.seq:.....  
GCATGCTTCATTATCTAATCTCCAGCCGTGGTTTAATCAGACGATCGAAAATTCATGCAGACGGTCCCAAATAGAAAG  
ACATTCTCCAGGCACCAAGTTGAAGAGGTTGATCAATGGTCTGTTCAAAAACAAGTTCTCATCCGGATTGAACCTTAC  
AACTTCATCCGTTTCATGTACAACATTTTGAAGCATGCTTC

## Clone Rv24

.....Rv24SP6.seq:.....  
ATACTCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACCACGCGCGGGTTCGGGCGCCGGGCGCCG  
GCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCACCGGCTGCGCTACGTCTATCCATACCGGGCG  
GAGCTACATCGGCTCGGCCGCCCATTTGTCNGGCCCTCTTTCGAGGTGAGGTCTATACCGATTGCGCATCCG

.....Rv24T7.seq:.....

TCCGTACTGGTCGGGTACGCTTCGGTCGCAGTGTGCGAGTGATAGATGACGACCGGGACCTCGTCGGCATCTTCCATA  
GCCCCGCACACCTTCAGTTGCTCACCAGGAATCCAACCGGTAGAAAGGTCGGCGAGCGCTCGGCATTGGTCATCGGGATA  
TGCCGCTCGGGACGGTCAGAACCTCGGGTCCG

Clone Rv251

.....Rv251SP6.seq:.....

GTTCTCGCACGATTTTCGGATTAGCGGGATGGTCTCAATTGGGTATGCGGGGAAGGCGCTGACATTGCGCCGCGATTAGC  
TGTTTGATGGACCGGGGGTGAATTTTATCAGGAAATGGGTGTTTATNCAGGTCGCACGCTTTCATCCGGGGCGGAA  
CG

.....Rv251T7.seq:.....

GGGTGTGCTGTGTATGCACGGCATACGGACATCCTTCCCCTGAAGACCCGCGGTGGAACAGCCACGTGTCCATC  
ATCANGGGGTCAACCCCGGCCAAGGGCGACGGCAGCCAAAGTTCGCCGACCGTTAACCTAGTGCTGTTAGCTTCATTT  
GCTGCGAGCAAAACAGCTGGTTCGGNCGTTAGGAATGAATTGAACTCAACCGATTTGGTGCCGCCGTAGGTGTCCTGG  
CTG

Clone Rv252

.....Rv252T7.seq:.....

ACTACCCGGCCAACGGTGATNTCTTGGCCGCCGCTGACNGCGCGAAGCAGCGCCAGCGACCACATTCAGCAGATGGCCA  
GCGCGTGCCGGGCCACGANGTTGGTGCTCGGCGGGTACTCCCANGGTGCGGNCGTGATCGACATCNTACCCGCCGCAC  
CACTGCCCGGCCTCGGGTTCACAGCCGTTGCCGCCCGCAGCGGACGATCACATCGCTTTATTTNNTNTTCNGGAAT  
CCCTCGGGCCGCGCTGGCGGGCTGATGA

Clone Rv253

.....Rv253SP6.seq:.....

ACGTCCGGANACTGTTTCGCGTTCATCCTCGTCTCGGCGGATTGGTCTGCTGCGCCGGACCGACCGATCTTCAGCGGGG  
GGTCACGCTCCGTGGGGTGCCGTTACTTCCGATCGCCAGTGTGCGCGTGCTGTGGCTGATGCTGAACCTCACCGCGT  
TGANTTGGATCGGTTCCGGATCTGGCTGCTGGCCGGAACGCNATTTATGTCGCTACGGGCGCCGGC

.....Rv253T7.seq:.....

GCTCAAAGGCACTACTGGCACCAAGGCCCACACGTACCTGTGACTCCTGCGCCGACCCGCCGAGGTCTGGCCGTTA  
CACCGAACGGCGAGCCGGGAGTTGGTACCATCGAACAAGACAAGGTGCATGGGCGGAGTTGTTCCGCCACTTCGTCG  
ATGACGGGTC

Clone Rv254

.....Rv254SP6.seq:.....

CGATACCGGCTGCTTACCGAGACATCCACCATGCCACCCGAATCACCGCACGCGCCGAAATCGCACAAACAGCTTGACG  
CCTTGACAGTTCCGCGATTGGAATTGCCGACGGTCTCTGACGGCGTCGACCTTGGCAGCCTCTACGAGCTCTCGGAAT  
CACTTGCCCGAGCAGGGGGTTCGATGAGTGTACACCCGAAGACCTCGATATGGGCGCAATCCTGGCCGACACATCCAAC  
CGGGTGGTTGTGTGCTGCGGCGCCGGTGGGGTCNGCAANACACTACCGCGGCGCGCTGGCGTTGCGCGCGGCCGAAT  
ATGGCCGCACTGTGGTTCG

.....Rv254T7.seq:.....

CGTCGTCGTCGTTGGTATGCGATAGCCATCCCGTCGGGCTACTCGCCATCACCGATCAGCTTCGCCCCGAAGCCGCCG  
GGCGATTTCCGCTGCGACCAAACCTGACCGGGGCCAAACCGGTATTGCTTACCGGCGACAACCGGGCCACCGCCGATCG  
GCTCGGTGTACANGTTGGCATCGACGACGTACGGGCGGGGCTACTGCCGACGACAANGTCGACGCCGTGCNGCNGCTG  
CAAGCTGGAGGTGCCAGATTACCGTGGTTCGGTGACGGTATCAACGACCTCCGGCCTTAGCGGCCGCGCATGTGCGCAT  
CGCCATGGGCAGCGCCCGAC

Clone Rv255

.....Rv255SP6.seq:.....

GCACGCAATCGAAGTCACCAAACCGGGCGGGCCAGGGCTCTNACGCCACGTGNACCGCCGAACCTCAACCCGGCC  
ACGGCGAGCTCCTGATCAAGGCGAGGCCATCGGTGTCTACTTCATCGACACCTACTCCGCTCCGGGCAATATCCGC  
CGGAACCTCCCGTTTCGTCTGCTCCGAAGTATGCGGCACGGTGGANGCCGTCGGCCAGGGGTTAC

.....Rv255T7.seq:.....

TGCACTGTGTGGCCACAGATCACGCCCCGCATGCCGAGCACGAGAAATGCGTCGAATTCGCCGCGGGCCGGCCGGCAT  
GCTCGGGTTGCAGACGGCATTGTGCGTGGTGGTGCATACAATGGTGGCGCCGGCTTGTGANTTNGCGCGATATCGC  
GCGGGTGATGAGTGANAACCGGCGTGCA

Clone Rv257

.....Rv257SP6.seq:.....

GAACCTGACACCCTGGTCACGGGTGAGCACGGACTTGATTTCTTCNCTATTGGTCGGCGCTGTTGAGCACACCACGCC  
GCTGACGGCCGTCGCGTCTCGCTGTGCTCGGTCTGGTGGAGCGCGCTGCCGCGGCCNAACATCNTAAATCAAGCGT  
ATTGCTCAACAGATATCATCAATGTGCGCGCTGGACTATTCAAATCATCGATATACTGGTGACCTGGTCCTTCGCCAT  
CGATCAATGGCGATAGTCACGCAAATCGTCACGGACATCGTCGGCGTCCCAGCTGGCCCGTGCCAACAGATGCTGCAA  
CCCATCGGGGTGGTATCACCGCGGTGCTCGGCATGGTCCACAATTCTTGCGGTCCAAGCCNAAACATCCCGGGCAT  
GAATTCACCGGCATGCGCN

.....Rv257T7.seq:.....

CTATCGTACCCGCGCCGGTCACCTTCTGGATATCGCCGGCCCTGGTCAAGGGGGCGTCCGAGGGAGCCGGGCTGGGTNA  
CAAGTTCCTGGCTCATATCCGCGAATGCGACGCCATTTGTGAGGTGGTGGGGGTGTTGCTCGACGACGACGTGACTCA  
TGTCACCGGACGGGTGATCCCCAGTCCGACATTGAGGTGCTCGAGACCGAGTGATCCTGGCAGATCTGCAAACCCCT  
GGAGCGGGCCACGGGCCGGCTGGAGAATGAAGCGCGCACCAACAAGGCGCGCAAGCCGGTCTACGAAGCGGCACTGCG  
TGCCACGANGTGCTCGACGCGCGGCAAGACGCTGTTGCGCGCGGGGTGGATGCCGCCGCGTTGCGCGACTGAAACT  
GCTGACCACCAAGCCCTTCTCTGT

Clone Rv258

.....Rv258SP6.seq:.....

TACTCAAGCTTCAGGCCGCCACGTCCGCCGTCCGTGCGCGACGTGACCTCGAGCGCCGAGTTCGACTCGACATCGCCG  
CCGGCGCATGCCGACATGAACGCGGCACTACCGCAAGCCCGTGGACGTGAGTTCGATCGACTCCGCTTCAAGCACC  
GGATCGTCCGGGCAACTCGCGGCCCTCGGCCTGTGCGAACGGCACACCCGTCGTGGCGGCNCCCCGCGCGGAAGTGGG  
TCATCAGGTGCTTGGAGCCGGTCCGCTCACCGCGTACCGACGCCGTC

.....Rv258T7.seq:.....

CCGACATCGAGTGGGCTCGCAGTGACTTGCGCGACCTCCAAGCCACCGGTACCCGCCGCGCGGCAAGCCAAGGACGACG  
ACGGCCTTGCCGGATAGCTGCGCCAGGCGTTGCGCCAAGTGGCGTCCAGCGTCGCCACGATCGTCAAAGAGCTTCATC  
TGCCGAGTGTGTCGCCATCTCATGGCTCCAAATATGGAATTAGGTCCCTGGGCCGACTGACGACAGTCCCTCAGCGAC  
CGGATTGCGCATCCCGCCTTGACGCTACTCCGCAAATCCCGGCTTGCCTCCGCGGAAGCGAACTCGGCGGCGCTAC  
GTGGTGGTTCACTTCGGCCGTGCGCACTCGGATCGACGGGCCGATGGTGGCCGGGCCCGCGCGCTTCTTGGTCATCCG  
ATTGAGT

Clone Rv259

.....Rv259SP6.seq:.....

ATACTCAAGCTTGTGCGGTAACCGCACGCAAGGCGGTGGGTGCGGTGTCAAAGACACCCACACTTCTTTGCGGTTTC  
GGTGATCTCGACACCGGCCGCGAGCCGACCAACCATGCGCGCGTAGATCGGCGATCAGCGCGTCGGCTATCGCCTGGGT  
GCCGCCACCGGAATCGGCCAGCCGACCGAATGGGCCAGCGTTGCCAGCATCAGTCCGGCGCCGGCCGACACCAAGTGA  
CGGCAACGGTGAAATCGCGTGGGCGGCAACGCCGTTGAACAACGCGCGGGCATCCTCGCCGCCAACGACCGCCAGGC  
AGGGTGCCTGGGCCATCATCCGACGCCGA

.....Rv259T7.seq:.....

TGGACTCATAACGATCGGGTCAGCGACGCGCAACACGAACGGCCGGACGAGTGGGCCAGGGTCGCGCCTCCCCTACA  
AACAGGATCCGTTGCCTGCGAGCGACAGGCTCCGGTGCGGCGTTGGGCGCCGTGCTCGTCCCAGCGTCCGGTCCCGGG  
TCGCGGCGACGCTTGTTTCTCCATACTCGCCCCCTAATCTCGAGGACAGCCGTACCCGACGGCAACCTCCCAAAA  
TGCAATCCCCCAAATGCAATGCGTCGAGCTATTTCTCACACCGACCGCTAGTTGCGGATCAGAAATCCGTTGGGCGC  
GGAAGTCCAGCCGAATTTGTTCTCCCGCTCCGCATCATGCTTGTAAATCGTTTGGAAATCATCCTCATATGCCTCGATC  
GCTTCATAGGTCAAGCCCAAACCCGGCAGGATGGGTGGCC

Clone Rv25

.....Rv25SP6.seq:.....

CTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATG  
ACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTAGTGTTGCGCACGTAAATTCGTCAGGT  
GACCGATCCCCTGCTGTCTCACTCGCCTCACAGCGACCACCAGGCTGGCGCTCAAGGCGGGCACGTGCGGAGCAGAT

GAGGAATGTGCGACGTCTTGATGCAGCCTGTGAGAACACCGAGACCTCGACGAACTTACGATCGAAACCGCTTAGGC  
CAACCGGTGACGGGGGTGTCTTCCGCGGCTAGGGCGCCTTATCGTCCGAAGGCCGTGGGTGGTGATCGCCTTCTGGG  
TCGCGCTTGCGGGTCTGCTTGCGCCGACGGTGCCGTCCCTGGACCGATCTCCAGCGGCATCCAGTGCGCATCTGCC  
ATCGG

::::::::::::Rv25T7.seq::::::::::::

CAGGCATGCAAGCTTGCGATGTATCAACACGCCGTTGCGCAGCGTGAGCCGATAGTTGACATCCGGCTCGGTGAAGGT  
GAAATCGATGGCCAGGTCGAGGTCCCATGCGCGTGGGCCATTGATGCTGATCGCCAGGACGTCAAAGATTTGGTCCGG  
CGTCAGCTGGGCGAAAAACGTGGGCGCCGGGACTTGCCCGGAGCTGCCGGGTTCCCGTCGCGCAGCTCGGCGGCCCC  
GGTCAGAAAGAAATTGCGCCAGGTCGCACACTCCGCGCCGTAGGCCAGCTGCTCCACGGTGTGCGCATATAGCCCCGCG  
GGCCGACGCTGCTCGCTGTGCGCGAACACCGCATGGTCGAGAAGCGTTGCCGCCAACGGAAATCACTGCGTCAAAG  
CTTCCGCGGGGCCACTCCAGCACTCCGTC

Clone Rv260

::::::::::::Rv260SP6.seq::::::::::::

ATACTCAAGCTTGACCGACGCTGATCGCACCGCACGCGGGAACCTCAAGGGCACTACTGGCACAAGGGCCCCACACGTC  
AACCTGTAACTCCTGCGCCGACCCCGGCCGAAGTCTTGCGCTTAACACCGAACGGGCCAACCCGGGAATTTGGGTT  
CCATCAAAACAAATAGCAGGTGCCTGGGCGGAGTGTTCTC

::::::::::::Rv260T7.seq::::::::::::

GTCGTGCTGTGCTGGGGCGTCCGTATCAGCACGCCACGAAATGGGGCACAAGAAGGATTCTTGAACGGTGGCTGTC  
CAAGATCACCTCGCCAAAACCTGCTACGGGCACTTCTACATCGAGCACAACCGTGGCCATCACGTCCGCGGTGTCCA  
CACCGGGAGG

Clone Rv261

::::::::::::Rv261SP6w.seq::::::::::::

ATATGCCTTGCTGAGCTTTTCGGATCGCAGCGAGTCGTACCCGCGCCGGTCACCTTCGTGGATATCGCCGGCCTGGTC  
AAGGGGGCGTCCGAGGGAGCCGGGCTGGGTAACAAGTTCCTGGCTCATATCCGCGAATGCGACGCCATTTGTGAGGTG  
GTGCGGGTGTTCGTGACAAACGACGTGACTCATGTACCCGGACGGTCGATCCCCAGTCCGACATTGAGGTCTGTCGAG  
ACCGAGCTGATCCTGGCAGATCTGCAAGCCCTGGAGCGGGCCACGGGGCGGCTNGAA

::::::::::::Rv261T7.seq::::::::::::

GACACCCTGGTCACGGGTGAGCAGGACTCGATTTCTTCGCTATTGGTCGGCGCTGTTGAGGCACAGCACGCCGCTGAG  
GCCGTGCGCTCCTCGCTGTGCTCGGTCTGGTGGAGCGCGCTGCCCGCGGCCGAACATCGTAAATCAAGCGTATTCTGTC  
AACAGATATCATCAATGTGCGCGCTGGACTATTCAAATCATCGATATACTGGTGACCTGGTCTTCGCCATCGATCAA  
TGGCGATAGTCACGCAGATCGTCACGGACATCGTCTGCGTCCCAGCTGGCCCGTGCCAACAGATGCTGCAACCCATCG  
GGGTGGTATCNC CGGTGCTCGGCGATGGTCCAACAATCTTGCGGTCCAAGCCCCGAAACCATCCGGCCATGAGTTC  
ACCGGCATGGCGCAACGGCTGGTGCCGGGCAAAACGCGGCGCGATCGAATTC

Clone Rv262

::::::::::::Rv262SP6.seq::::::::::::

TGTAGAAGGTGGGTCCCGTCCAACCTTCGCGGGCGGCGCGCATATGCCTTGCTGGTCTTGCTCATTTGATATCCAATC  
TATGGGTGCTGGTTACTCAACGGGCCGAAGCTGGCCCTCCACGGGTAGGGTCTATTCGACGGTGATGTCC

::::::::::::Rv262T7.seq::::::::::::

CCCGAATCCGGTGGCCGGCAGGGGCGCTGGCGACGTGGACACCTTCTAACTTGTCTTTACCGGTCACTGTTGCACCCC  
AACACCTTTAACGACGTGGACGGACGTTACATCGGATTCGACGGTGTGATCCACAGCGTTGCCATTGGGCACACCCAC  
TACGCCAATTTCTCGACTGGGACACCTACCGCAGCCTCGCCCCACTGCAGGGACTGTTGTTCCCGCAACGGGCCATC  
GACATGATCCAGTCGTTGGTGACCGACGCGGAGCAGACTGGTGCGTATCCGCGTTGGGCGCTGGCGAAATTCGCCAC  
CGGCATGAT

Clone Rv263

::::::::::::Rv263SP6.seq::::::::::::

TTGAGATGCTGGTCGGGATGCCGATGGTTGGAACATGGTCCCCTGGCGTCGAATACGCGCGAGCGCATGAGCTCACCG  
GTTCCGGAACAACGTATCGAAGAACTCGCACTGCTGGCAGATGGTATCTCCGATGTGGTTGTAATTTGTATCCCAACTC  
TAACTGTGCTATCGGATCTGCGTGAATA

.....Rv263T7.seq:.....

CGTAATCACGATCCCGCTGAGACACTTGACCTTACGGCCGAAGTGACTTCGCTGCTGCTATGCCGACACCCGATTTC  
ATACGCTGCTGTACACGACGGCCGGCCGGTGGCCCTCCATCACGCTCAACCGCCCGGAACAGCTCAACACCATCGTCC  
CGCCCATGCCCGACGAGATCGAGGCCGCTATCGGGTTGGTCGAACGCGACAGGACATCAAGGTCATCNTNCTGCGCG  
GTGGCGGGCGCGCCTTCTCCGGCGG

Clone Rv264

.....Rv264SP6.seq:.....

CAAGCTTAAGCTGGTTCGGGCCACTCCATGAGCCGTAGTGCAATGGTTTCGTGCACGGCGAGGCCGAAGTTGCCATAAA  
CATCCCTGACGAAAGTCTCCGGCAAGCCGATTGCTTCTTCGGGCCGCTTCTTGTGGATTGTCCGATAACCCGGTCCCT  
CATGCTGGAAGTTGTGCGCACTCTTCTCCGCGATGTGGGCTAACGACTCGTCATTGAGCAAGAAGTACGTGCACA  
GGCATCGTCCGCCGGGCTTCAGCACGCGGGAGATCTCGTCCAGATAGTGCTCCACGTCCGNGGGAAACATGTGGGTG  
AACACCGAGGTNAGAAACACNCATCCAACGACGCATCCGGGATATGGAAAGCGAAA

.....Rv264T7.seq:.....

TATGGTCTTCGTCGACCAGTACGTCGTAGGCGCCATGAGCCAGCGACTGAAGCCGCGCCATGCCTGCACGGCCCGCTC  
ATCCAGCGAGGCGGCCATCTCCCGCAGATAGCCTGCCGCTCGGCGCGCACGCTGTCCGGATCGCGTCCGAGCTCGTC  
GGCCAGCGCAGCGACGCCGCTCGTCATACCATCGGGCATCCAGCAGTTGGGTAACTCAACGGGGTTCGGTTCGCTAGCGG  
CGTCATTGATTACGCAACAATACCGATGCGCTGCAGCAACTTTCGAGTCCGATGCGGCCACCTCCCGTGCAGTCAC  
TGGCTAGCCCCCGTCATGCCGTTGTGTGATGGCACGGCAGCGGGCTCGTAACTGCGGTCTCAGCTCGCTGG

Clone Rv265

.....Rv265SP6.seq:.....

GCTTAGCGGTCTTGCTCGAACCACATTCGCTGCCACTCATGAGCGGGTGGCGGTTCGCGGTGCTTACACATCT

.....Rv265T7.seq:.....

GTATCTGGCGCTCTCGAATATCCTTGAACGTCCCGCGGTGCCACCCAGATAGATCGCAGCGCCCTGCAATGGAGTTC  
CCTTTATGGCCTCTCTAGCCTCCCGCTTGATCGGCTCGACCCGAGAGATGCCCTCGGGCGTTGCGGGATCTCCCTCCA

Clone Rv266

.....Rv266SP6.seq:.....

CTTCACGCCGATCCGCGACCGCGAACGCGACGGTGACGGTGGGCGACAAGGTTTCGGTTGGTTCGCCGCGGGCGCTGGGCG  
ATATCAGCTCACCCGGTTTCGAGGTGTTCCGGCGACCGGACGGTGCTGCAGACATTCTTGAGCGTCTCGACCGGCCCG  
ATTCCGCCCTTCAACATCGTGACGCCGTATTTCCGGCGGTACCGCTCGGCGCCGAGTCAAGGCGGCCTGAGCTAAAGCC  
GGGCATTGCGCGAGTGGTAAACAAGTTCCGTTGACTTCGGTTGACCGACTCGACGGGCTCGATCTGGGCGCGCTGGACC  
GGTATCTGCGTTTCGCTGGGGATCGGGCCNACCGCNANTTGCCTTGCANCTGATTCCGGTGGAGCTCCAATCTGACTT  
CCGG

.....Rv266T7.seq:.....

GCAGCTACCGACCCTAGCGACGAGTGTGTTTCGACGCGTCGAATGTGAACGTTTCGGCGTGATTTCGGCGCGCGGGTTCCC  
GCTCTCAGCGCACGTTTCGGCGCCGAGGNGGCTAGTCCCTGGTTAAGCAATGTCTCGGTTCGCCGCCAGCAGCGCGCATG  
TCGCCAACCCGTCNACCGCGTTGCGCATGTCCGGTACCGACGGAACGACGGCGCGATCCGGATGTTCTTGTCTGCTCCG  
GATCCTTTTCGATACGGGAACGACCCCGCCTCGGTACCCGCGATACCAACGTCCTTAGCCCAANGCTACNGTCCGGCG  
CGCGGTCCCGGGCAACACGTCAAGCTGATGAANTAACCACCCTTGGGCTCGGTCCAAGANGCGATCTTGGACTCCTT  
AACCGCTGATNCAA

Clone Rv267

.....Rv267IS1081N60.seq:.....

TCCCCATCGGCGCCGGACCGTTTGAAAGTCCAAGCACGGGTGGGATGGAATCGACGACAGTTGAGCGCCGTCGGTGGC  
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AGGAAGATTGACGAATCCCTCGCAGGCGCGGCACGTCCGCAGGCCAACGCCAACTACGGGGCCACCAGCGATCCTCCG  
CTCAGCACCAAGCCAGGCTCANCCACCAAGTCGGCCCGCGCTCTCCCTCGCCCCCTGGTCTCCGGGGCCTT  
GTTAAACAATAACCGGAAGTCCACCAATCCTCGCTGCATCTCGACACCGTCCGCCTCACTCCCTTCTCCCGCCCTC  
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.....Rv267SP6.seq:.....

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ATCACGGTGGCGGTAGCCGTTGCGCTGATTGGACCGCTCATCGCTGCGTTGCGGGTAGCCCGCCCCGCACAGGGCGTC  
GGCTTCAGCCCCCATCAAGGCGGCGA

::::::::::Rv267T7.seq::::::::::

GGCCGAGTCCAGCACTTCGCACTATGTGCAGACCAANACCCGGTGGTCGCCGCGCTGCGGCAGCGGGCTGGCAACGGC  
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TCATCAGGTATCACGTGTCGATGACGTGAGCGTTAACTTCCCCGACCAGACGGCGACCTCGCCGATGGACCCCGCT  
TGTACCTGGTGTGGGCGCAAGCTAACGCCGCCGANGCTATCGGTACTCGGTGCAAGCGCAGCCGGGGTTCGCAAGCGC  
TAGCGGGCAAGGTGCGGACGATCTCGGTACCTGGACCAACTACGGCGCTGCTGCCGCCACCGAATAGTNGTGCCCCG  
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Clone Rv268

::::::::::Rv268SP6.seq::::::::::

AGCTTCAAGGACATCGTCAATCGCGACCAAAACCGCGAGCTAGGTGGGCATCCGGGAAGCATCGCGACACCGTGGCGCC  
GAGCGCCGCTGCCGGCAGGCGGATTAGGCGGGCAGATTAGCCCCCGCGGGCTCCCGGCTCCGATTACGGCGCCCCGAA  
TGGCGTCACCGGTGGTAACCACGCTTGC CGCCTGGGCGCGGGCTGCCGGATCAGGTGGTATATGCCGACAAAGCC  
TGC GTGATCGGTCAACACGGTGACAGCAGCCGGTTGTGCACCATCGCNAACGCCACCCCGGTCTCCGGGTCTGT  
CAN

::::::::::Rv268T7.seq::::::::::

GCTCGCGGTCCAGCAGCAGACGTGTCTGACCCCGACGCCCGGCCCGGTACCGAAACCGGATCGGCCCGCCGATGGC  
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CAAGGTGATTCGGCGTGGCGGGGTTTCGCGAATCGTCCACCGCCACCACCATGCGGGTGCTCTCGAAGACGCGGGGC  
TGTGCGGGAACAGCGAGTTAATGTGGCCCTCGGGCCCCATGCCAGCAGGTGGACGTCGAAATTTCGGCCCGGGTCACC  
TGGTGGGCACTGGCGGCC

Clone Rv269

::::::::::Rv269SP6.seq::::::::::

AGCTTGTGATCGTCCGGCAGCGTCCGGCGAGTCAAGTGAAGCCAGTCCGGTCTCCTCTCCGACTACGGCCAAGAAC  
TGGGCGACGGTGTGAGTGCATACCAGCGGANACTGGTGGCGCCCTAGGCGAGCGACCGCCTCACAAACGGCGGTGACC  
GCGTTCTGGTGTGACCATCGAGCCGTGCCATCCCGGCCGCGTCCGTGAGCCGCATCCACTGGATGCCCTTCTCG  
GCGGTTTCAATCAGGTACAGGCGACGTTGCCANCATCGTGCCGGGGCANGG

::::::::::Rv269T7.seq::::::::::

TTGGTGATCATCGNCCCAACGACCCCGAGGCGATGTTCTTGACACCCGAGGAGTGTGCAAGCTGGGGCTGGCCTTCG  
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TTCAACCAACGACTACTAATGGGATCTGCTGCTGTCCAAGACCGGCTGGTCAGANGCCGATGTGATGGCGCAGATCGAC  
CTGCGGGTGACCACATTGGGTCTAAGGGTGTGATTGGTAGAACCTGACGCACCACCATCCACGTGCGCGTTGGTC  
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Clone Rv26

::::::::::Rv26SP6.seq::::::::::

GGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAAGCT  
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TGGTTATCGTGGGTACCGTCGTGCTTTCCATGGGCGCCTCTTTCGGGCTTTCGTTATGGTCTGGCAGGACATTCTGG  
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TGATTTCCCGGTTGAAAGAGGAAATTGGGGCCGGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGGAG  
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::::::::::Rv26T7.seq::::::::::

CAGGCATGCAAGCTTGGCGTGCCGTTCCAACCCGAATTGGCTTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTC  
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CAACGCCGCGCGGAACGTTCCGCCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGAC  
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Clone Rv270

.....Rv270SP6.seq:.....

GGCATCTTGGCCGCCATGTTAGCCACACTGCCACCGGCTATAGAAGCGATGCGCACCGTCCTGCCAGCACATTGCGGC  
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.....Rv270T7.seq:.....

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CGATGGCCCGCGCGCTGCTGTTATCGGTCCATTCCGCAACGACTAGGGGTGTCCCCGCCGGAGCTGATGCCGTGAC  
AATGGCACCCACCTCCTCGGTGGGGTGGGCACCGTGATCGCGAACCCACTTCATCACCGCAGCCGCGGCACCTTGGC  
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Clone Rv271

.....Rv271SP6.seq:.....

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GAGCCGAGCGCCGTGAGATGTACGACCGGGTGGTCTATGTGCCGCGGTTGGTGAGTTTCCACGACCTGACCATCGAAG  
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CCACCGTCGG

.....Rv271T7.seq:.....

CCTAGGTCAACCGTACCGTCATCGGATCGGGGTGACCGGCACAGATGGACTGGAGCTTCGGCGAGGTGATCGCCTATG  
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CTCAGGCCACCGGAAATCATTCGCGGGTGGCTGCACGACTGCGACGTGGTACCCTCCAGGTGCAAGGGCTGGGCGA  
GACGATGCAGACCGTCCGGACGAGCGGCACTCCTTTTCCGTTGGCTCTTCGGCCGAATCCGGACGCCGAACCCGACCG  
GCGCGGGGTCAACCCGGCACCGACGCGGGTGCCGTTTACCCGCGGGCTGCACAAATCCCGACGGGTATGGGCTTTGAC  
CTGCCGACGGGGGA

Clone Rv272

.....Rv272SP6.seq:.....

AGCTTGGCGTGACACCAACACAGGGCACTTAAGATGGCAATGCGCCGCCTACCTGCACGTTTTTCGCGATGTCAGAGGA  
TGCCGAGGGGAGAACAAATGCGAGCACGGCCGCTGACGTTGCTCACCGCTTTGGCGGCGGTGACATTGGTGGTGGTTGC  
GGGCTGCGAGGCCCGAGTCTAGGCCGAAGCATATAGCGCGGCCGACCGCATTTCTGCTCGACCGCAAGCGCGACCTCA  
GCCGCAGCCGTTGGAGCTACTGCTGCGCGCCATCACGCCGCTAGGGCTCCGGCGGCGTCGCCGAACGTGGGTTTGG  
CGAACTGCCTACCCGGGTCCGGCAGGCAACCGAT

.....Rv272T7.seq:.....

TCATGCCGTTGGACCGACCATCGGAGTTAGTTGCCGAACCGCGGGACACCGCAAGCACCCGGTCCTGGTCGCGCACC  
GCGTCGGCCAACCGCTTGAGCACCACCACGCCGACGCCCTCGCCGCGCACGAATCCATCCGCGTTGGCGTCGAAGCTG  
TTGCATCGGCCGGTGGTGACAGCGCCGACCACTTGACAGCGCGATGGCGGTGAACGGTGACAAGGTGAGCTGCACC  
CCGCCCCGAATGCCACGTGCTTTCACGCAGGCGAAGCTCTGACACGCCAAGTGAATTGCCACCAGCGACGACGAAC  
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Clone Rv273

.....Rv273SP6.seq:.....

GGGTCGACTTTCTGCAAGGCGAGGCTACACCGTCGTGTCGTGGTATGCGATAGCCATCCCGTCGGGCTACTCGCCAT  
CACCGATCAGCTTCGCCCCGAAGCCGCCGTGGTGATTTCCGCTGCGACCAAACTGAACGGGGCCAAACCGGTATTGCT  
TACCGGCGACAACCGGGCCACCGCCGATCGGCTCGGTGTTACAGTTGGCAT

.....Rv273T7.seq:.....

AATCCGAAATCCTGACCGATACTTGAACCTGGTCTCGTTTCCGGCAATAACTCGTCGGCGTGACGACGCGGCGCAAACG  
TACTTCGGCATCAACGCGTCCGACCTGAATTGGCAGCAAGCGGCGCTGCTGGCCGGCATGGTGCAATCTAACAGCACG  
CTCTTCCCGTACACCAACCCCGACGGCGCGCTGGCCCGGGCGGAACGTGGTCCTCGACACCATGATCGAAAAACCTTC  
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Clone Rv274

.....Rv274SP6.seq:.....

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CCATGGCCGAGCTGAACAGCTCGCTGTCACAGCTGAACAGCACCGTGGAGCGCTTGGAGGACGGTCTGGACCATCTCG  
AAGGTACCCTGCACAGCCTGGACGATCTCGCGAAACGGCTCATCGTGTGGTTCGAGCCGGTGGAAAGCCATCGTCGATC  
GGATCGACTACATCGTGAGCCTCGGCGAAACGGTGATGTCACCGCTGTCCGGTC

::::::::::Rv274T7.seq::::::::::

NCTCGATCTTGGGGTACGTTTCGATGAGGCTGCTGACCAACAACCCGGCCAAGCGGGTGGGACTGGATGGATACGGATT  
GCACATCATCGAGCGCGTGCCGCTGCCGGTGCCGGCCAACCGGGAAGAACATCCGTTACCTGATGACCAAGCGTGACA  
AATTGGGGCAGCACTTGGCTGGGTGGACGATTTTCACGAATCCGTGCATCTGCCCGGAGAATTCGGCGGTGCCTTGT  
GAAGGTGGCGCCGGGGTGCCGGATCTGCCGTGCTGGATCGTCTGGTGTGCGGCTGGCGATTGTGCCAGCAGCTGGC  
ACGGAAGATCTGCGACGCGCTGTTGGACGGCGCCCGCAAGTGGCCCGCGGTGTGGCCTCGATGACCGACTGTGGTT  
CGGGTGCTCCGCGCATCGATAT

Clone Rv275

::::::::::Rv275SP6.seq::::::::::

TCATCCCAGCAAAACGCGAGCTAGGTCCGCATCCGGGAAGCATCGCGACACCGTGGCGCCGAGCGCGCTGCCGGCAG  
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ACCGCTCTTGCGCGCCTGGGCGGCGGCTGCCGGATCAGGTGGTAGATGCCNACAAAGCCTGCGTGATCGGTCTATCAC  
CAACGGTGACAGCAGCCGGTTGTGCACCAAGCGCGAACGCCACCCCGGTCTCCGGGTCTGTCCAACCGATCGACCGCC  
CAAGCCCACATGAACAAACCCCGCATCACGTTGCCGATCGGCATACCGTGA

::::::::::Rv275T7.seq::::::::::

TTGGCGGGTTGGCCCAGCAGCCCGCCGGTGACGGCGACGATGCTGGGCTGGTTGCGGCCCTGCGCCACCGCGGCTTGC  
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CCGCGCGGCTCGACGAGTTTTTGGCCTGGACTACCCGCGTGGCCAATCTGCTGAACCTCGCGGCCGTGGTGGCCTGGA  
ATGTCGAGCGCCGTTACCTACGTGACCTGATGGATCGGGGGGTGCCGACCGTGCCCGGCGATGTGTATGTGCCGGAN  
AGCCGGTCCGGTTGCCACGCAAGGCCATGTCTTCGTGCGTCCGACCATCGGTACCGGGACACGGCGCTGTATTGCC  
GGTTGCTGCGCGAGTTGCTGCGCAACTGCACGCNGCGGGCCAGCGGTGCTCGTTCANCCCGAGGTTCCGGTGACG  
ATGATCGTGTGGTCTCCCT

Clone Rv276

::::::::::Rv276SP6.seq::::::::::

GTAGGAGAGAAACAAAGACCGTCGATAGGACACGTGTTACGCCGCTAGCTGTCATTGGTATGGGGTGCCGCTGCCGGGG  
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TGGGACATCTACGAGTACTACGACCCCGAACCCGGCGTGCCCGGACGCACCGACTGCAATGGGGCGCGTACCTCGAT  
AACGTGCGCGACTTTGATCCCGAGTTCTTCGGGATCGGGGAGAAAGAAACGATAGCGATCGATCCGACGACCGCTTG  
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GGGGTT

::::::::::Rv276T7.seq::::::::::

CGAAGTACGCCCATAGAAAGGCGAGCTAATTCGCTGGGCAATAGGAAGACCCCTTTGTCTGCCACGTATATTTGT  
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GATGCTGCCGAGCGCCCGCCACGATACGACGCCATCGCGCCTTGCGCCGCGTCTTCGACCACCGCCAGGTTGTGGTG  
CGTGGCGATCTTCATGATCGCGTCCATCTCGCAGGCCACCCGGCATAGTGAACGGGGACCATGGCCTCGGTTCCGCGG  
TGAA

Clone Rv277

::::::::::Rv277SP6.seq::::::::::

CTTAGACGCCACCTCCGGGCGGAGCTCCACGGGGTGGATAAGTACGGCCGGATGTGGCCGCAATGGGAAGTTGTTGCC  
CGCTTGACTGTCCGGTTAACGCCGATTCCACCACATCCCTTGCGAAAGGCCGTTGGGTT

::::::::::Rv277T7.seq::::::::::

GATCGCGATCGTCGATGTGGCCATCCGGCTTGGCGTCGACCCGCGTAAGGCAGACCAGATGGTTCGCGGCACGGTCAA  
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ACCGGATT

## Clone Rv278

.....Rv278SP6.seq:.....  
AGCTTACGCCGCTTTTCGCTTCNGATTTGGGACGCCGCATCGAAAGCGCAGTTGGAAGCGCGCGCGCCGGCTGGTCGAG  
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.....Rv278T7.seq:.....  
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CTTCGTCGGGGTGGTCGCGACCGCATGGGCCACATCGCATTCACCAGGTCGCGCGAATCACCAGCACGTANACGGTT  
CCTTTCCTAAGCAACACCGAAATTTTCAGGACCCGAATGCTCCGGGAAAACATGTCACGGTAAGTCCGGTATTCCGGGT  
ACCGGTTGAGCATTGA

## Clone Rv279

.....Rv279SP6.seq:.....  
CGGCATCGGTTTTGGGCTGTACCCAGCAGTTGGTAGTTCTTCACTACTGTTGTTTCGAGCGTCGAGCCGCCGCGCGTGT  
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TCTTCAATCGAGACNATCGCCAGCTTCATCGTGTGGCGATCTTGTCCGAGGGCACCTCGAACCGGCGCTGCGANTAC  
AGCCACGCGATCGTGTGGCCTTCGCGTCGACCATCGTCGATACCGCAGGCACCTGCCCCCTCGAGCAGCTGGGCGCAT  
CCGTTGGCAACGACCTCAGAGGCACGATTGGACATCAGCCCTAGCCCGCCTGCG

.....Rv279T7.seq:.....  
CCGTCGANGCCGCCGACTTGGCTTGACCGACACCAACATGGCCTGAGGGTGTTCAACAAGACCGTGGCCGACGGGCTG  
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GAACGGTCGAGGTGCTCTACACCGAGTATTCGAAGTCGAAAGGCCAACCCTGCTCAACGGCGTCAACATCATTTTCG  
ACGGGTTTCTGCGAGGGAGGATGCCACGATGAAGTGGATCCAGGTGCTGTTGATCGCGTCGATCATCGGGTTGCTGTT  
CTACCTGTTGCGGTTCGCGCCGAAGCGCGCGGTCCGTGCCTGGGTCAAGTGGGCTATGTCCTGTTCTGCTCCCGGCA  
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## Clone Rv27

.....Rv27SP6.seq:.....  
TTACACGNCTGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGAC  
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CAATTTACTAGCGAGAGTCTGGCCGATNCGGATCTGACCGAAGTCGCTGCGGTGCAGCCACCCCTCATTTGGCGAT  
GGCGCCGACNATGGCGCCTGGACCGATCTTGTGCCGCTTGCCGACGGNACGCGGTANGTGGTCAAGTCCGGTCTACN  
CTTGGGCTTTTGGCGACGGTCCCGACGCTGGTTCGCGGTTGCGCCGCGGAAAGCGCGGGTCCGGTGCCATCAGGAATG  
CCTCACCGCCGCGGCACTGNACGGCCAGTGCCGCGCGGATGTCNGCCATCGGGACATCATGCTCGCGTTCATACTCCT  
CGACC

.....Rv27T7.seq:.....  
CAGGCATGCAAGCTTTGTACACCAAGTGTTCGACCAGGCGCTCCATCCGGCGAGTGGATACTCCAGCAGGTAGCA  
GGTCGCCACCACGCTGGTCAGTGCAGCTTCAGCTCGCTTGCGGCGCTGCAGCAGCCAGTCCGGGAAATAGCTGCCCTG  
GCGCAGCTTGGGGATCGCGACGTCGATGGTTGCGGCACGGGTGTCGAAATCACGGTGGCGGTAGCCGTTGCGCTGATT  
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## Clone Rv280

.....Rv280SP6.seq:.....  
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TACCTATCGAGCAAGACAGCCCGTTTTCGACAAGATGACTTTTCGGATCTCTTCGGCGACTTCGATGGGGTCGTCGG  
GAGTCCCAGGGCGCCACCGCGAGGTAAGCCTCGTCCCAGCCCCATACCTCGACCGGGTATCCCAGGTTCGCGCAATAACG  
CCACCACCTCCTCGGACGCCGCGTTGTAGGCGGTGGGTTTCGACGGCAAGAAGTGGCCTCAGGGCATCGTCGGCGCGG  
TCCCAACGGCNTGCCGGCGCGCACACCGTAGGCGCGGGGCTC

.....Rv280T7.seq:.....  
CCGGCGGAACTCAGACGTGCTGGTGGTGGCGCATGGCACCGCGGGCAGCAAAGCGCACTTCTCCGGGGACGACAGCAA  
GCGACCGCTAGACAAGAGGGGTCTGTCGCGAGGCAGAAGCGTTGGTACCACAGCTGCTGGCGTTTCGGCGCCACCGATGT  
TTATGCCCGCCGACCGGGTTCGCTGCCACAGACGATGGAGCCACTCGCCGCGGAACTGAACGTGACCATACACAACGA  
GCCACCCCTGACCGAAGAGTCTACGCCAACAACCCCAAACGCGGCCGACACCGAGTGTGTCAGATCGTCGAGCAAGT

AGGCACACCCGTGATCTGCACGCAGGGCAAGGTCATTCCCGATCTGATCACGTGGTGGTGCGAGCGCGACCGTGTGCC  
CCCGACAGTCCCGCAATCGCAAAGGCAGCACGTTGGTGT

## Clone Rv281

::::::::::::Rv281SP6.seq::::::::::::  
GTATGGTCAGCTGTCCATCCGGCGCTGTCGGCCGAGCTGCCAGATCTCGTCAGCCGTAACCGGGTTGCGGGATCCACG  
CGTGCGGGTTGTCTAC

::::::::::::Rv281T7.seq::::::::::::  
CCGACTTTCCGCGGGTACCCGCTCAACTTTGTGTGTCNACCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAAC  
ACTTCATCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACT  
ACATCATTCGCACGGGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACC  
TGTTTCAACCAAACCTTGAAGGTGATTGTTAACCTGGGCTACGCGACCCGGCCTATGGTTATTTCGACCTCGCCGCCAA  
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## Clone Rv282

::::::::::::Rv282SP6.seq::::::::::::  
GCACCGATGTCGGCGAGCACTTCGTCAACTTCCAGGGGTGCCCGCACCAAGTATTTTCGACGAGTATTTCCGTCGGGCC  
GCCGCCGCCGGTGC GCGGCAGGTGGTCATCCTGGCGGCGGGGCTGGGACTCGCGCGCGTACCGGCTGCCTCGGC

::::::::::::Rv282T7.seq::::::::::::  
TGCACCCAACCTTACTGAGCATGCTAACGCTGGTCTGTCGGGGTCTTGTTCGCCGCTGTCGGCAGGGCACACGCTCGGGG  
CGTAGCTGGGAGAGGCCCCGGTCAAGCCCGGAGAGCAGTGCTCAGTCCGCCAGCTTGACCGACTTTTCGATGAGAACGC  
GCTTCTCGCCGATTTGAAGTGGCGTGCTGACGGTCGCTGAGCAGCGCTCGCCGAGTGC GGCCGCTGATTCTTTTCATCG  
AGCCAGGACGCGCATTCGTGTTTCGGCCGC

## Clone Rv283

::::::::::::Rv283SP6.seq::::::::::::  
AGCTTACGGCCGGTCGACGCGACGAGTGGTTCATGACACCACAAACCGTCAACGCCTACTACAACCCGGGGATGAACG  
AAATCGTCTTCCCGCAGCGATTTTACAGCCACCATTTTTCGATCCGCAGGCCGACGAGGCCGCCAACTACGGCGGGAT  
CGGGCGCGTGATCGGGCAGCATGATCGGGCACGGTTTCGACGATAGGGCGCCAAATACGANGGCCGACGCAATCTGGT  
CNATTGGTGGATCGA

::::::::::::Rv283T7.seq::::::::::::  
ATGTCGTCACGTCAACACAATCGCGAGGACCCAATCATGCCGCCAGGGCGGCCAACCCAATGGTGGCCGCGAAGCGG  
CAGCTCGATCGCAGCGCGGAGGTGCCGGCCGCCAGTTGATTACGAACAGGGTGAGGTATAGGCGGGCAGGATAGTG  
ACGAACGCAAGACCTATATCTGCCGTGCGAGTAAGAATCGAGTAGCCGGTCGACCAACGGAAGCGAAAGTGTCCGCGA  
TGTTGATGAGCGTCGCCGTTGTGGCGGCGGTGGC

## Clone Rv284

::::::::::::Rv284SP6.seq::::::::::::  
AGCTTACACGCGTGCCGATGCTGTTGTCNACACCTCCCTACTATGCGCAATTCGCCGACACGGGTGGCATCAACACG  
GGCGATAAGGTGGACATCGCTGGGGTGAACGTCCGGCTGGTGCGCTCGCTGGCAATCCGCGGCAACCGCGTGTGATC  
GGATTCTCGTTGCCCGGCAAGACAATCGGGATGCAAAGCCGGGCAGCAATTCGCACCGACACCATTCTTGGCCGTAAG  
AACCTGGAATCGAACCCCGCGTTTCGGAGCCGTTGAAACCAACGGTTTCCTGCCGTTGGCGCAGAACTACGCCA  
TACCAAATCTATGACGCGTTCGTC

::::::::::::Rv284T7.seq::::::::::::  
CTGCCGCGGTGGCGGTGACGCGCTGGCAAGTCACCGCACCGCCGTCCGGTTCATCGGCAGGCTCCCCGAAAAGGGCC  
CTGGCAACAGAAAGGTGATCAATGAGCTCCCGCAGACCTTCGCCGATCTGGGACCGACATACGTGAAGTTCGGCCAGAT  
CATCGCGTCCAGCCCGGAGCATTTCGGTGAGTCGCTGTGCGGGGAATTCCGCGGCCTGCTCGACCGGGTGCCGCCCC  
CAAAAACCGACGAGGTGCACAAGCTCTTCGTCGAGGAACTCGGCGACGAGCCGGCCCGGCTGTTGCGCTCCTTCGAGG  
AAGAACC GTTCGCTCTGCTCCATCGCCCAAGTGC ACTACGCGACCTGCGCAGCGGCGAAGAAGTGTGGTCAAGATC  
CACGGCCGGGCATCCGCCGCCGCGTTT

## Clone Rv285

::::::::::::Rv285SP6.seq::::::::::::

GATCGTGCCGGCCCCCGGCGGCAGTAGCAGATCAGCTCGTCGAAATCGCGGCAACCAGTCCAGTTCGATTTCCATACG  
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CGGGATCGGATGAATCATCAATATTATCAAGTGATTTCTGATGGCATCGAGCTCGGTGATCTTGGTCTCGGGGGCCA  
GCTCGCCGTCGGCGACGTCGTCGATCCGGCGGCCGAGCGCATAGACCGCAAATAGTCCGCTCGCTTTTCGCGCGGCA  
AGAGTCGGATGCCGTAATATANGTTTCTGGCGGCCGTGCGCGTGATCNACTCGGTGATTCGATACGCCTGTTTCATCTC  
GGTCATGCCGTCCTC

::::::::::Rv285T7.seq::::::::::

GGTGGCGCAATGACCGAAACCACCCAGCCCCGCAAACCCGGCGGCCCGGGCCCGCACAATCGTTCGTGTTG  
GAGCGGCCCATCCAGACCGTTGGGCGCCGTAAGGAGGCCGTGGTACGAGTGC GGCTGGTGCCCGGCACCGGCAAGTTC  
GACCTCAACGGCCGAGCTTGGAGGACTACTTCCCAAACAAGGTGCACCAGCAGTTGATCAAGGCACCCCTGGTCACC  
GTGGATCGGGTGGAAAGTTTCGACATCTTTGCCACCTGGGCGGCGGCGGCCCGTTCGGGTGATGGCCGGCGCGCTGCG  
CCTGGGTATCGCCCGGGCATTGATCTNGTATCGCCGGATGACCGGCCCGCGCTGAATAANGCCGGCTTCTTGACCGT  
GATCCACGCGCCACCGAACGCAA

#### Clone Rv286

::::::::::Rv286SP6.seq::::::::::

CACAATAGATTACTCAAGCTTCAACCAGCGGCCTTATCACGTATCCCCGCTGAGACCTTGACCCTTAGGGCCGAAGT  
GACTTCGCTGCTGCTATGCCGACACCCGATTTCAGACGCTGCTGTTACACGACGGCCGGGCGGTGGCCACCATCAC  
GCTCAACCGCCCGGAACAGCTCAACACCATCGTCCCGCCCATGCCCGACGAGATCGAGGCCGCTATCGGGTTGGCCGA  
GCGCGACCAGGACATCAAGGTCATCGTGCTGCGCGGTGCCGGCCGCGCCTTCTCCGGCGGTTACAACCTTCGGCGGCGG  
GTTCCAACATTGGGGGCAT

::::::::::Rv286T7.seq::::::::::

TCAGGACGCTTATGGTTGGCAGATGGTCGCCCTGGCGTCGAATACGCGCGAGCGCATGAGCTCACCGGTTTCGGAACAA  
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ATCGGATCAGCGTGAATATCGAGATATTGCGAATGCGATGACAGGCCGCCATTTCGGTTTATTTCGCTTACGCTTCCCGG  
GTTTCGATTCTGATGCACTGCCGCAAACGCGGATATGATTGTTGAAACCGTATCTAACGCAATTATTGATGTGGT  
AGGCGGCAGCTGCCGTTTTGTGCTGTCCGGCTATTTCATCGGTGGGGGTGTTTGGCTATGCCCTCTGCTCCCAT

#### Clone Rv287

::::::::::Rv287SP6.seq::::::::::

CGCAGCTGTCGCCGATCTGGTCCGGAATACCTAGCTCCAGGTTCTGAGTGGAGATGAGTGCGGCCATCGAAGTGTTGT  
CAATGTACTCCAGGATGTCAGGTGCCAGGCCGCTGGCGAGGATCTTGGGCACCGCCGCCATGACTTGGTTCGAAGTCGG  
CGAACGGGGCGAGCACGCTGGCGTCGTGGTC

::::::::::Rv287T7.seq::::::::::

GTAGTTCGTTTCATCCAAACACAGTGCGGTACCGGCTCAAGCGGATCACCGACTTCACCGGGCGGATCCCAACCCAGCC  
ACGCGATGCTTATGCTCTTCGGGTGGCGGCCACCGTGGGTCAACTCAACTATCCGACGCCGCACTGAAGCATCGACAG  
CAATGCCGTGTCATAGATTCCCTCGCCGGTCAGAGGGGGTCCAGCAGGGGGCCCCGAAAAGATACCAGGGGGCGCGTC  
GGACCGA

#### Clone Rv288

::::::::::Rv288SP6.seq::::::::::

TCCGCTCGTTCTCCGAGAGGTTGAGTGCCAACGCTCTGCCGATGCCCGAAGCCGGCCCCGGTGATGACGGCGACCTT  
GCCTTCGAATGAGCTCATTTGACTACTCCCCGTGGTTGTCCCTGCGATTGGTGGAGGTGGCCGCGCAGCCTTGCCCCG  
AGGTGCGCGATCGCGTCTCGGGCTTCGGGGAGCAGACTGACCTGCAGATGGAAGTCGTGCCACATGCCCGCGAACCGG  
CGATGCTCGATGCTTGTTCGAAGCGGCGCAGGCGGTTTCGATCTTGTCCGCTCAACACNGATCGGATCGTCGCCC  
GCGGTCTGCATGACGAATGGGCG

::::::::::Rv288T7.seq::::::::::

ATGGGAGGCCACCGATTACCATCTTGACACACCGATTCCGGGCTATTGATGTCCACGTTCCGGTCCGCGAACCGCGCT  
GTGGCTGCTGCTGGCCAAAGGCGGAGGCGATACCGAAGTCAGTGCCCAAGCTTGGGTTCCACGCTCGCGCAGCCACGC  
CGTCACCTTTCCACGAGACCTCACCTGCCGATCCGAAATGGAATCGGCCGTGACGGAATTGGCGCAGCGAACACTCAA  
CGAGGTGGTGGCTTCGTGCGGAACCGTCACCCGAGTCGCGGTCAACGTCGCGACGGCGACGTTCTACACCCGCAACAA  
GATCCGAAAGCTGCAAGCTCCAGCACCGATCCCGACGTCATCACCGCTGCCGCCGGCACGTTCTTGAACCTATTTCG  
AGCTGGAATCGGCCGTCCGGTTGCTGGGAATTGCNGTTAAGAACTGGGCCT

## Clone Rv289

.....Rv289SP6.seq:.....  
GCTTTGCGCGCTTCTCCGAGAGTTGGAGTGCCAACGCTCTGCCGATGCCCCGAGCCGGCCCCGGTGATGACGGCGACC  
TTGCCTTCGAATGAGCTCATTGACTACTCCCCGTGGTTGTCCCTGCGATTGGTGGAGGTGGCCGCGCAGCCTTGCCC  
CGAGGTGCGCGATCGCGTCGCGGGCTTCGGGGAGCAAACCTGACCTGCAGATGGAAGTCGTGCCACATGCCCGCGAACC  
GGCGATGCTCGATGCTTGTTCGAAGCGGCGCAGGCGGTTTCGATCTTGCCGCGTCAACGCAGATCGGATCGTCGCC  
CGCGGGTCTGCATGAAGAAT

.....Rv289T7.seq:.....  
CTCACGCAGCCACGCCGTACCTTTCCACGAAGACCTCACCTGCCGATCCGAAATGGAATCGGCCGTGACGGAAATTG  
GCGCAGCGAAACACTCAACGAGGTGGTGGCTTCGTGCGGAACCGTCACCCGAGTCGCGGTACCGTGCGCACGGCGAC  
GTTCTACACCCGCACCAACATCCGAAAGCTGCAAGCTCCAGCACCGATCCCGACGTCATCACCGCTGCCGCCCGGCA  
CGTTCCTTGACCTATTTCGAGCTGGATCGGCCCGTCCGGTTGCTGGGAGTGCGGTTAGAAACTGGCCTAGAAACCGGCGG  
GCACACCGCACCTGGGCGGGG

## Clone Rv28

.....Rv28SP6.seq:.....  
TGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG  
CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCCGCCAGCCACC  
ACNCGCGGGTCGGGCGCCGGGCCCCGGGTGCCANGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCACCGGC  
TGCGCTACGTCGAGCCATACCGGGCGGAGCTACATCGGCTCGGCCGCCAGTGTTTCGGGCCCTCTTCGAAGTCGAAG  
TCGATACCGATTGCGCATCCGCNGCCGCA

.....Rv28T7.seq:.....  
CAGGCATGCAAGCTTCACGTCCGTACGGCTCGGGTACGCTTCGGTTCGCAGTGTGCGAGTGATAGATGACGACCGGGAC  
CTCGTCTGCATCTTCCATAGCCCGCCACACCTTCAGTTGCTCACCAGGAATCCAACCGGTAGAAGGTGGCGAGCGCTC  
GGCATTGGTCATCGGGATATGCCGCTCGGGACGGTCAGAACCCTCGGTCGCGCCAGCACTCCGCAGGCTTCGTGGG  
GTGGTCGCGACGCGCATGGGCCACC

## Clone Rv290

.....Rv290SP6.seq:.....  
GCTTGCTATCGTCCCAGGTCAGGTCCGGCCAGTCAAGGTGCAAGGCCAGTCCGGTCTCCTCTCCGACTACGGCCAAGA  
ACTGGGCGGACCCGACAAATCGATGGCGCGCACATCGCGTTTGCCAGGTGATTGCTAATCCGGTCGGGGTCAAGTT  
CCGCGTTCTGGTCGTGCACCATCGAGCCGTGCCAGCCCGGCCGCGTCCGTCAGCCGCATCCACTGGATGCCCTTCT  
CGGCGGTTTCAATCAGGTACAGGCGACGTTGCCACCATCTGTCCGGGGCACGGTTAGCGAGAAACCGCCGACTTCAC  
GATTGCCTCGGTGATGCCGTCGAAACAGATCGGGCT

.....Rv290T7.seq:.....  
GCGCGCCATGTTGAGGTTGTCCGACGGTGACGACGGTGAACCACAACCTGTTTGACCTGTCCGCACACACCGTGTGGAT  
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GGGCCCCAACATGACCCCGGAACTGGCCGTGGAGTACGTGAGCGGCTCGACCCGCACAATAAGCCGGGGCCGGCTGAC  
TTGGTGAGCAGGATGGGCAACCACAAGGTCCGCGATCTGTTGCCACCGATCGTGGAGAACGTCCATGCCACCGGGCAT  
CAGTCATCTGGC

## Clone Rv291

.....Rv291SP6.seq:.....  
TTGCCCTTCCATGCCGAGCAAGGTCGACTCAGCGATGACGAATTGTTCTTCTTCGCGGGTGTTGCTGCTGGTTGCGGGC  
TATGAGAGCACTGCTCATATGATTAGCACATTGTTTCTGACGCTGGCCGACTATCCAGATCAGCTGACACTCCTTGCG  
CAGCAACCAGACCTGATCCCGCCGCGATCGAGGA

.....Rv291T7.seq:.....  
CGACGCTGGGCCCAACTGCGACCACAGGTCCTGGTATGGCAGGACATGGCCGGGTTACGCGGCGCAATACCG

## Clone Rv292

.....Rv292SP6.seq:.....  
TAACGACTCGGGTCCAGCGACCGCGCAACACNAACGGCCGAGGTCGCGGCCCTCCCCTACAAAC  
AGGATCCGTTGCCGACGACAGGCTCCGGTGCGGCGTTGGGCGCCGTGCTCGTCCAGCGTCCGGTCCCGGGTGC



## Clone Rv296

.....Rv296SP6.seq:.....  
GCCCCGTTTCGATCGGGCATGTCCGAGTCGTCTTACCGGAGGCGGTCTGGCCGCGCTAATCGGCGTCGGCGCCGAC  
AAGATGTGGGATATCCGCAATCGGGGCGTCATCCCTGCGGGCGCGCTCCCCGCGTCCGAGCCTTCGTTCGACGCAATC  
GAGGCAAGTCACGACGCGGATGAGGGGCGAGTGAATTACAGCGAGGTCGAGCTGTTAGTTCGCGCTCATCAACTGT  
TCGCCGGAAACAGTCGGCGACCGGGGTTGGATGCGGGCACCACACCCTACGGGGGATCTGCTGTCTCGGGCTGCCGAC  
CTGAATGTNGGTGCGGGCANCGCCGTATCNACTCCCGTGGAACACAGCCGGGGC

.....Rv296T7.seq:.....  
CTCGGCGTGGATATCGGTGTAGCCGGCGCCGGTGAANGTCGGCTCCTTACGTCCACTCGACAACAGCTCATAGCGATC  
CAACCACTANGCAACCGCCTTCAGCAGTACAACCGCGCCGGCGAACACTGCGAGTTGAACGCGAGCTGCCTGGGTTCAG  
CATGCTCTGCCGTTGTTCAGCCGAAGGCCGCCGAACAGGTAATGCGTCAACAGGCTCGCTAGAAACGCCAGAACCAC  
GGCCACGAACAGCCAGTTTCAGCACCGACCGGTAGAACGGCAGATCGAAGACGAAAAACCAATGTCATAGCCGAATT  
CGGGGTCCACGATGCCAAAGGTGCCCCCGTGTACAACAACCTGAACCTTCACCCA

## Clone Rv29

.....Rv29SP6.seq:.....  
TCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAA  
GCTATTTAGGTGACACTATAGAATACTCAAGCTTCACGTCCGTACGGCTCGGGTACGCTTCGGTTCGAGTGTGCGAGT  
GATAGATGACGACCGGGACCTCGTCGGCATCTTCCATAGCCCGCCACACCTTCAGTTGCTCACCAGGAATCCAACCGGT  
AGAAGGTCGCGGACCGCTCGGCATTGGTCATCGGGATATGCCGCTCGGGACGGTCAGAGCCCTCGGGTCCGGCCAGCA  
CTCCGCAGGCTTCGTTCGGGGTGGTCGCGACGCGCATGGGCCACCATCGCATTACCAAGGTCTGCGCGAATCACCAGCA  
CGTAGACGGTTCCTTTCTAAGCAACACCGAAGTTTCAGGACCGAATGCTCCGGGAAACATGTCA

.....Rv29T7.seq:.....  
CAGGCATGCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACCACGCCCCGGTTCGGGCGCCGGGCC  
CGGGCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCACCGGCTGCGCTACGTTCGAGCCATACCGG  
GCGGAGCTCCATCCGCTCGGCCGCCAGTGTCCGGGCCCTC

## Clone Rv2

.....Rv2SP6.seq:.....  
CCTGCATCCGGCTCGTATGTTGTGTGGAATTGTGANCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTA  
CGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCCAATCCCCCTGCCCTGATACGCGTCGGCAACCGTGAA  
CGCGATCTCGGCGACCGCTCGGATCGGTTTCATCCCGCACAAAACGCGCGTCGGCTACGGGGTTCGCTTCGCTCGGTTCAC  
CACCCAGACGAAGTGGTCGACGTAGTCGACTTCCGACAGGTAGTGCATCAACGCCGGACTGGGAACACNAGCCGACAT  
GAACCGTCGATACAGCGTCTCNCCGGAGAAGTGGATGTGTCCGTGCACGGTCCGCTCGCGGTACCGGGCAGCACGGG  
GCGTAACATCAGTTGAGTCCCGTCGGCAAGCCGTACCGGAATCGGGGAGACGA

.....Rv2T7.seq:.....  
CAAGATGATCGCCGGTGCCACCCCGATCCGTGCCTCGGTACGCGCGAACGTGCTTTCCGGTCCGGCGACCAACCATGTCT  
GCACGCACCGACAGGCCGAACCCGCGGCCCGCACATGCCCGTTGATGGCGCCGACCAACCGGCAGCGGCGACTCGAC  
GATGGCGCGCAACAGCGCCGTATTTCCCGCGCCCGCGCCACCGCCATCCGGTACGGATCACCACCACCAACCGCCGGC  
CTCGCTGAGGTCCGCGCCGGCGCAGAACGTTCCGCCGGTATGCCCCAGCACGACCGCCGACCGCCGGATCTGCTTC  
GGCCGCACTCAGCCCTTGATGTAGTTGGCTGACCAAGCGTGCTCGACAGCGCGTTGCGGTTGTGCGGAGAGTTCAAGTGT  
CAGCCTGGCGAAGGGGCCCGCGAGGCGGCCGGGCCAGCGTAGTCGACGGGGCTG

## Clone Rv301

.....Rv301SP6.seq:.....  
CTCAAGCTTCGATCGACAGTACTCCGCGCTTGGGTCTGGTCTTCGAGCTGGTTCGGTTCATGGTTCGGACCTGCTGGTAGT  
GGGGATCTAACGCAACATGGTTCGGGATTCATCATGGTGTACCCGTGATACCCATTTCGAGCTGCCGGTGAAACCCCGC  
GATGCCGGGATTTCCAGCCGCACTAGGATGTCTAGCCGGCCAGCCGCTGCCGCCGGACTTCGGGATGTTCCGGTATACC  
ACCGATCGGCAATCTTGCTATCCGCCGATGCTCGAAGCGTAGCCACCCCAAACCAACCACTGTGACNACAATC

.....Rv301T7.seq:.....  
TGAATTTCCCGATCCCAATCTCGGTTTCAGATACAGGTTCGCCATACCCCTTACTTCGGCAACGCTGGGCGGATTGGC  
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GCCGATCGACATCCCGGCCCTCCACTATCAACGGAATTTTCGATGTTCGGAGGTCTGCGGATCGATGTGTCCGTTCGACAT  
TCCGG





GGGCATATGTCCANAACGGACGNGGCCGGTTTCNTCGATGCNGCCGGGGTCCGCGACNTGCGGACNCCNCGNCACACC  
ATCCGCCAGTCCGCGTGGCGTCCCGCCGCGACTCTGCCTCGGCCGCGCCA

## Clone Rv310

::::::::::::Rv310SP6.seq::::::::::::  
CTCAAGCTTTGNCGACGATCGGGCGATGTCGATGANAGGAAACCCAGCGCACAACCGACNATTTTGGCGTAGCCGGC  
GGACNTCTGCTCGATTCCGATCACGTGCGCGCTCGCATCGAGCATGGCGCCGGCGACGGCTAGCAGCGATCCGCCGTC  
GTCGAGGAACACGACACGAGCCGTACGCCCGGCCGTAAGCCGCGCCAGGATTCGGCGAAAAACCGTTCTACGTGGCG  
GGTGTACTGGGTGTCCAATGATTCTGTGGGTGCGTAGGCGTCGCTGCAATCGTCGACATAAATGCCGTCGGCCCGCAT  
CGCGTCAACAACCTCCCGGGTGAGTGGAATANCACTTGCCGA

::::::::::::Rv310T7.seq::::::::::::  
TCCAACGCGGTGACAGATTTGTCTATCCTGGACCTGACGGTGAGGTGCAAGTTTCCAGGAATTCGGCAAAATCGGTA  
AGAGCCTGAAGAATTCGGTATCGCCGGACGAAATCTGCGACGCATACGGGGCAGATACGCTTCGGGTTTACGAGATGT  
CGATGGGGCCGCTGGAGGCTTCACGTCCATGGGCCACAAAGGATGTTGTGCGCGCGTACCGTTTTCTGCAGCGGGTGT  
GGCGCTTGGTCTGTCGACGAGCACACCGGCGAAACTCGGGTGGCTGACGGCGTGGAACCTGCACATCGATACGCTACGGG  
CGTTGCACCGCACCATCGTCGGCGTGTC

## Clone Rv311

::::::::::::Rv311SP6.seq::::::::::::  
CTCGTCCTTGACTACGCCCAGTATCGAAANCCTCCTGTGCCGGTNCGCTAAACACCCGGCGGACACTCANACGGTGCT  
GGTGGTGCGGCATGGCACCGCGGGCAGCAAAGCGCACTTCTCCGGGGACGACAGCAAGCGACCGCTAGACAAGAGGGG  
TCGTGCGCAGGCAGAAGCGTTGGTACCACAGCTGCTGGCGTTTCGGCGCCACCGATGTTTATGCCGCGGACCGGGTGCG  
CTGCCACCANACACTGGAGCCACTCGCCGCGGAACTGAACGTGACCATACACAACGAGCCNCCCTGACCGAAGAGTC  
CTACGCCAACAACCCCAACGCGGGCGACACCGAGTGCTGCAGATCTTCG

::::::::::::Rv311T7.seq::::::::::::  
GTATCGCCTCCNCCTTTGGCCACCAGCAGCCACAGCGCGGTTTCGGGACCGAACGTGGACATCAATAGCCCGGAATCG  
GTGTGTGCAAGTTGGTAAACGGTGTTGATCCCAAGCTTTGCCAGCCTTTTCGTAGTCTTGGGCCCCACACCCACAGT  
GCTTCGACGGTACGGTCACCCATGATGGCCATCCAGTTGGCATCGGTGAGCTGATAGATGCCAGCTGGTTTCGCCAAC  
CCGGTAGCGATCTTGGCGCGCTGCTTGTGTCAGTATACCTATCGAGCAAGACAGCCCGGTTTGGCACAAGATGACT  
TTTCGGATCTCTTCNGCGAACTTCCAATGGGGGTCTCCGGGANT

## Clone Rv312

::::::::::::Rv312SP6.seq::::::::::::  
CTCAAGCTTTTGGTCTAGCCGGCCGAGCACGATACGGGTGTCCTTGCCACCGGCGGCGGCTGTCCGGGAAATGGCGG  
GTCCCCGGTGTTTGGTGANGANTGCTGAACCGTAGTCGAAGTGGGCGGCGTCAGACTCCACCCAGCCAGCAGGCAG  
CGCGAAGCTGAATCCTCCAACCGGGTTGTGATCCGGACAGGTTGGGGTGCCTTTGGGGCAATGACAGGTGGCGGCGG  
TGCCTTCGGGTTCGGCCGGCGGAGGTGCTGCGTTGGGATCNCCTGGGCTGGGCATTGCGCNTNTTGGCGGCGGCGGTTG  
TGGGGGGCAACANGTGTCCCGGTGCGGGTGGCGTGCTC

::::::::::::Rv312T7.seq::::::::::::  
ATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCGCCGACTTTCGCGGTACCCGCTCAACTTTGTGT  
CGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAACCTTTCATCCTGACGCGGGAACAAATTGACGCAG  
CGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACTACATCATTGCGACGGAGAACCTGCCGCTGCTAG  
AGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGTTCAACCAAACCTGAAGGTGATTGTTAACC  
TGGGCTACGGCGACCCGGCCTATGGTTATTTCGACCTCGCCGCC

## Clone Rv313

::::::::::::Rv313SP6.seq::::::::::::  
CTCAAGCTTGCAATGCGGGTCGGGATGCCCATGGTTGGAANATGGTCGCCCTGGCGTCNAATACGCGCGAGCGCATGA  
GCTCACCGGTTCCGAACAACGTATCGAAAAACGTGCGCACTGCTGGCAGATGGTATCTCCGATGTGGTTGTAATTTGTA  
TCCCAACTCTAACTGTGCTATCGGATCAGCGTGAATATCGANATATTGCGAATGCGATGACAGGCCGCCATTCCGGTTT  
ATTGCTTACGCTTCCCGGGTTCGATTCTGCTGATGCACTGCCGCAAAACGCGGATATGATTGTTGAAACCGTATCTA  
ACGCAATTATTGATGTGGTAGGCGGCAGCTGCCGTTTTGTGCTGTCTCG

.....Rv313T7.seq:.....

CAAATACACGCCGGACGCACAGGCGGACATCGCCATCCCGAGCACACCCAAAACGGGATACAGGATGGAGGCCAACGC  
CACGGCCGCGCCAGGATCACCACACACCGGCTTGGTCAGCTTGTGCGCGGCGGTATAGGCATCGGGCCGCTGCAA  
CGCAGCATGCACAAACGCGTACACCGCTGTACCAAGACGGCGACCAGCAATACCAGCATGACGGTACCCACGAGGTG  
GCTCACGCATTAGACTATGCGGTTTGCATCCAACACG

Clone Rv314

.....Rv314SP6.seq:.....

CTCGTCCTTCGGCCTCGCTGCAGGAGTGGGAGCCGCAGGGCTGGAAATCCGAAAAACGAGCCGGTGATCGCACTGTGCG  
CCGATCGGCGCCGCACCTGGTTGGTGTACGGATGAATCCGCAGCGAAATGTGGCTGCGGTGGCGTGTCTGACTCGT  
TGGCGTCGACGCTGGTGGCAGCCACCGAGCGGTTGGTCCAGGATCTGGATGGGCAAAGTTGTGCGGCCCGCGGTGA  
CGGCCGATGAGCTGACCGAGGTCGACAGCGCCGTGTTGGCTGACTTGGAACCGACATGGAGTCGCCCCGGTT

.....Rv314T7.seq:.....

GTCTAGNCCGCGGAACACGATACGGGTGTCATTGGCCACCGCGCGGCTGTCCGGGAAATGGCGGGTCCCCGGTGGT  
TTTGCTGAAGANTGCTGAACCGTAGTCGAAGTGGCGCGGTCAGACTCCACCCAGCCAGCAGGCAGCGCGAAGCTGAA  
TCCTCCAACCGGTTGTGATCCGGACAGGTTGGGGTGCCTTGGGGCAATGACAGGTGGCGGCGGTGCGTTCCGGTC  
GGCCGCGCGAAGTGCTGCGTTGGGATCGCCCGGTGGGCATTCGGCGTGTGGCGCGCGCCGGTGG

Clone Rv315

.....Rv315SP6.seq:.....

ACTCAAGCTTGAGATTGGCGTCAACGGGTGTCGGCACCGGCGTCCTGCAGTTGGTAGGCCTGCAGTTTGTGCATCAGG  
CCGATGCCGCGGCCCTCGTGGCCACGCATGTACANACCACGCCGCGCCCTCACGGGCGACCATCGCCAGCGCGGCG  
TCCAGCTGAGGCCCCGAATCGCAGCGGCGTGACCCAAACACATCGCCGGTCAAGCACTCCGAATGCACCCGGACACG  
ACGTCG  
TCACCGTCGGCGTTGGGCGCGGATCTCGCCGCGGACCAGCGGACATGTTCCACGTCTCGTAAATGCTGGTGTAN  
CCGATGGCGCGAAACTCCCCATGACAANTCGGAATCCCGCGCCTCGGCGACCCCGCTCAATGTTGCTTCTCNTGCTTG

.....Rv315T7.seq:.....

TCGACNAGCATTCTTGACNGTTGTTTTGGCTCGGCATGGTTAGCCAAGGTTCTGCGGTCCCACCAGATCATCTTGGTC  
CGGTAGCGCTCGTCCGGGTATGCTGCCGCGGGATTCTCGTGTCTATTACTCCCCCGAAGAACGCCACCGGTCCAGC  
GCGTGGGCGCGCGGTTCCCATCACAACTGAACCCCCAACAGGGGACATGCTTAGCGGTAGGGCGCGCGCCAAGGC  
GGCAGCAATCGCATCACTGCGCTGCGCGTCACTATTAACCCACCCGGACTTCACTTCCACGACCCCGAATGGCGCCCG  
GTCATTGATCATCTTGCGCACCGCGGATAATCCGGGAT  
TG

Clone Rv316

.....Rv316SP6.seq:.....

ACCGGGGCCACTCCGCACAATCTGTACCCGACCAANATCTACACCATCGAATACGACGGCGTCGCCGACTTTCCGCGG  
TACCCGCTCAACTTTGTGTGNACCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTTTCATCCTGACG  
CCGGAACAAATTGACGCNCGGTTCCGCTGACCAATACGGTCGGTCCCACNATGACCCANTACTACATCATTGCGACG  
GANAACCTGCCGCTGCTAAAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGTTCAACCAAAC  
TTGAAGGTNATTGTTNACCTGGGCTACGGCGANCCGGCCTNTGGTTATTCCACCTCNCCGCCCAATGTTTGCNACTCC  
CGTTCGGGGTTGTTCCCNNAAGGTCAACCC

.....Rv316T7.seq:.....

CGCTCAAGCGCNTGAGGCCGAANCGGCTGGTTACGACTCCCTGTTTGTGATGGACCACTTCTACCAACTGCCCATGTT  
GGGGACGCCCCGACCAGCCGATGCTGGAGGCCTACACGGCCCTTGGTGCCTGGCCACGGCGACCGAGCGGCTGCAACT  
GGGCGCGTTGGTGACCGGAATACCTACCGCAGCCGACCTGCTGGCAAAGATCATCACCACGCTCGACGTGGTTAG  
CGCCGGTCGAGCGATCCTCGGCATTGGAGCCGGTTGGTTTGANCTGGAACACCGCCAGCTCGGCTTCGAGTTCGGCAC  
TTTCAGTGACCGGTTCT

Clone Rv317

.....Rv317SP6.seq:.....

CTCAAGCTTGCGTTTCGATGAAGTAGTCGTGCGTCAGCGCCGCTCTTCGAGCTCCTTGGCGATGCCAGCAAGGAGTC  
ATCGCCGCCGAGCTTGTCAGGATCTTGTGCGCCTGTTCTTACGATGCGGGCCCGCGGATCGTAGTTCTTGTAGAC  
ACGATGACCGAAACCATCAATTTGACCCCGGCTCGCGGTTCTTGACCTTGCCTACAACTCGCTGACGTGCTCGCC

GCTGTCGCGAATGCCCTCGAGCATCTCCAGGACAGCCTGATTGGCGCCGCCATGAAGCGGACCCCATAGTGC GTTGATGCC

.....Rv317T7.seq:.....  
GGTCAGGCCGAGCAGGCGCGAGGAACGACGAACCCAACAAGCCATGGTGGTTGGCGCCGTCGAGAGGTTCGGCGGTTCGC  
CACAACGGGAAGATCGCCTTGAGCGTCGCTCGACCGCCGCCCTCGAGTTGGGTCATAACGAAGTAGCTGATGCCGATCA  
TGTCGACGTTTCCGTCGATCAGCGTGCAGCGGCGACCCACTCNACGAGGTCTCGGTGCCGCCGCGGCCAGGGCACCA  
GCAGTGACGAGTCCAGGCGCCGTCGGGCCAAGCAGTCGCGGTGCCANCCGTGGTGGGTTCGGGCGATGGTTGGGTGTGC  
TCATTTCCGGGAACGCCA

Clone Rv318

.....Rv318SP6.seq:.....  
CTCGAAGCTTTAACAGCATCAACCCCGCCCCGACCCGACCCGACACNATGTCGATGCCATCGAGGTGAATGTGGAAC  
TGGCGCAAACCATCGGCGACCGCGACCCGCGCAACATGGGTACCGGCGATTTCGGGTGCCAATGCCGACCCGACGGG  
CCGCTCTACCGCAGGTGACCTCGATCACCGAGACCANCCGGCCGTTNTNNTCACGCACCCCTACCGTGTACGCCCCA  
AAACGGCGCTGGTGGTCGATTGCCGGAGTGACCCCNACCCAGTGTCTGTCGCCCGATCC

.....Rv318T7.seq:.....  
TGATGCCGCAACCGATCGACGGTCGTTGGTCGGGGTTGACTGGCCGCCCGCGAAGCAGGGCGTCGACCGCGGCCCGG  
ACGTCGGCGGCCGTCACCGGTTCGGCCATTGCCCGGGCGGGAGTCGTGAGCTGACCACGGTAGACAAGTCGGCGCTGG  
CCGTCGAAGACNAACGTGTGCGGTGTGACGGCCGCGGAGAAGGCGCGGGCGACNTCTTGGGTTTCGTCTANAGATAC  
GGGAACGTCCAGCCGTGGCGCGGGCCCTCGGCGACCATCTGATCGGGCCCGTCC

Clone Rv319

.....Rv319SP6.seq:.....  
TTTCGGGCGAGGCGGTATANCTTCCNCTCGTACCGGCGACCGCCAGCCGANAAGCTCGTTTCCCAGTGTTGCTGGGG  
ATTCTCACGCTGCTGCTGANTGCGTGCCAAACCGCTTCCGCTTCGGGTTACAACGAGCCGCGGGGCTACNATCGTGCG  
ACGCTGAAGTTGGTGTCTCCATGGACTTGGGGATGTGCCTGAACCGGTTACCTACNACTCCAAGCTGGCGCCGTCT  
CGTCCGCGAGTTCGTTGCTTGCATAGCCGGGAGGCCCCGGATCCGCAATGACGGATTCCNTGCCANCGCTCCGAGTTGC  
NTGCGGATCGACTACNAATTGATCACCCANAACCATCGGGCGTNTTACTGCCTGAAGTACCTGGTGCGGGTTCGGATAC  
TGCTATCCGGCGGTGACAACCCCGGCAAGC

.....Rv319T7.seq:.....  
GTTTTGGCTCGGCATGGTTAGCCAAGGTTCTGCGGTCCCACCAGATCATCTTGGTCCGGTAGCGCTCGTCCGGGTATG  
CTGCCGCCGGGATTCTCGCTGCTATTACTCCCCCGAAGAACGCCACCGGTCCAGCGCGTGGGCCGCCGCGGTCCCCA  
TCACAACTGAACCCCAACAGGGACATGCTTAGCGGTAGGGCGCGGCCAAGGCGGCAGCAATCGCATCACTGCGCT  
GCGCGTCACTATTAAACCCACCCGACTTCACTTCCACGACCCCGAATGGCGCCCGGTATTGATCATCTTGCGCACCG  
CGGATAATCCGGGATTGCCAGCCCATTCNACTACCGCATGCGAGTCATCGGCTGACCGCAGCGGT

Clone Rv31

.....Rv31SP6.seq:.....  
TCGCCTAGGCGGGCTTCCCCTTCCGTCCGAGCNGTCAGAAGCTCCTATGACAATGCACTACCCGAGACNATCAACGGC  
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GTCGATGGTTCAACCATCGCCGCTTACCGGTACTGCGGCGACATCCCGCCGGTCTAAGTCGACGCCGCTCACTA  
CGCTCAACGCCAGAGACCANCCGCCGGCTGACGTCTCAGATCAGAGAGTCTCCGGACTCACCGGGCGGTTTCATCCCC  
ACTGTGATAGCGTCTGTGGATAACTTTGTCTGCA

.....Rv31T7.seq:.....  
GCGCGTNGAACTGATAGGTGCGGCCCGGCTCGAGCANGCCGGCCATTTGTTGATGCGGTTACCGAAGATCTCTTCGG  
TGACCTGCCGCCGCCCGGCCAGCTCGGCCAGTGCCCGGCGTTGGCCGCCGCGGCGACAATCTTGGCGTCCACGGTGG  
TCTGGGTCA

Clone Rv321

.....Rv321SP6.seq:.....  
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CACATGACGAAGGGAAAGAGAAGGAAATCAACTGTGACAACTGCCCTCAAATTTGGCTTCCTTAAAAATTACAGTTC  
AAAAAGTATGAGAAAATCCATGCAAGGCTGAAGGAAACAGCAATAACTGTGACAAATTACCCTCAGTAGGTGAGAACAA

ATGTGACGAACCAACCTCAAATCTGTGACAGATAACCTCAGACTATCCTGTCGTCATGGAAGTGATATCGCGGAAGG  
AAAAT

Clone Rv322

.....Rv322SP6.seq.....  
CTCAAGCTTCGATCGACATTACTCCCGCCTTGGGTCTGGTCTCCGAGCTGGTCCGTCATGGTCCGACCTGCTGGTAGT  
GGGGATCTAACGCAACATGGTCGGGATTTCATCATGGTGTACCCGTGATACCCATTTCGCAGCTGCCGGTGAAACCCCGC  
GATGCCGGGATTTCCAGCCGCACTAGGATGTCTAGCCGGCCAGCCGCTGCCGCCGGACTTCGGGATGTTCCGGTATACC  
ANCGATCGGCAATCTTGCGTATCCGCCGATGCTCGAACGCTANCCACGCCAAACCAACCACTGTGACNACAATCGCCA  
CCACACCAAAGGTCATGCCCTCGGCGTGATGTCCGGTGCCGAAAGCCGCAAGAGCTCCGACGCCGCC

.....Rv322T7.seq.....  
CATTCCCAATTGAATTTCCCNATCCCAATCTCGGTTTCAGATACAGGTCGCCATACCCCTTACTTCGGCAACGCTGG  
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TCGACATTCCGCCGATCGACATCCCGGCTCCACTATCAACGGAATTCGATGTCGGAGGTCGTGCCGATCGATGTGT  
CCGTTCGACATTCCGGCGGTCAACATCACCGGCACCGAGTTCGACCGGATTCGGCTGAACTTCGACGTTCTCAGCAGCG  
CCGGACCCATCAACATCTCGATCATCGACATTCGGCGCTGCCGGGCTTTGGCAACTCGACCGAGCTGCCGTCTCGG  
GCTTCTTCAACACCGGCGGCGGTGGCGGCT

Clone Rv327

.....Rv327SP6.seq.....  
CTCAAGCTTTTCGGCGGAGACGGACANNTTGCGAACATTGATGACAAAATAGAAATCATTGATGGTTTGAGTCACCAGG  
CCGATCAAGCCTTCGCCGAGCCAAATTCCAATCAAGAGGCCCAAGCCCGTACCAATCAGCCCGGCAACGAGGGATTCC  
GTCATTATCAGCCAAAATAACTGCTCTCGGGTTACACCCAAACAGCGCAATATGGCGAAAAACGGTCGCCGTTGCACG  
ACATTAAATGTCACGGTATTG

.....Rv327T7.seq.....  
AGCTTAACTGCTCCCTAATACCTGGGGCTGTGCCTGCGGTGTATGCACGGCATAACGGACATCCNTCCCTGAGACCCN  
CGGTCTAATCAGCCACGTGTCCACCATCAGGGGTCAACCCCGGCCAAGGGCGACGGCACCCCAAGTTCGCCGACCGTT  
AACCTATTGCTGTGAGCTTCATTTGCTGCGAGCAAAACAGTTGGTCGGCCGTTAGGAACTGAATTGACACTCAACCGA  
TTTGGTGCCNCCGTAGGTGTCTGGCTGCGGGTGCGTGGTGTTCGCCGCTGTGGTAACGACCACAATGTGACCGGG  
GGAGGTGCAACCACTGGCCACGCGTCCGCGAATGTCTATTGCGGGGG

Clone Rv328

.....Rv328SP6.seq.....  
CTCAAGCTTGGGGTGGCGCTGTTCGGTTCGGTGTGCTTGGCGGCGTCGGTATCAACACCGCCACGAAATGGGGCACAAG  
AAGGATTTCGTCGGAGCGGTGGCTGTCCAAAATCACCTCGCCAGACCTGCTACGGGCATTCTACATCGAGCACAAC  
CGTGCCCATCACGTCCGGGTGTCCACACCGGAGGACCCGGCGTCGGCGCGGTTTCGGCGAAACGTTGTGGGAGTTCCTG  
CCCCGAGTGTTATCGGCGGCTTGCCTCGGCGGTTCAATTTGGAGGCCAACGGCTGCGTCCGGCTCGGCGTCAGCCCC  
CT

.....Rv328T7.seq.....  
GCACCAAGGCCCCACACGTCAACCTGTGACCTCCTGCGCCGACCCGCCCCGAGGTCCTGGCCGTTACCACCTGAACGG  
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GGGTCNATCCATTTCGAGGTCCTCGCCGCGTCCGGTCGAGTGGCGGTCACACTCCAGGTACTCGACCTCACAGACGAGA  
GGACTCGATCCCATCTAGGTGTGGACGAAACAGATCTTCTGTCCGA

Clone Rv329

.....Rv329SP6.seq.....  
TCGCTCCGCATATGGGTCGACGCCAAGCGGGTCCGGAATTTCTGGGCTTCATCGCTCGCGCCGTCCGCGACAAACAGCG  
CGGTCGAACCGACACTCGTTGTGATGTCCCAGCTATCACCTTCGGTACGCACCCAATCGACCCTACNCGGCTATCTCA  
GCCGCGATCTCCAGGCTCCGCCGAGCCAGGTGCATCCCGGTCCGGATCCCACTAACCCGGCACCATTGGCGTCN

.....Rv329T7.seq.....  
GTCTTCGAGTGCCGCCGTTCGNACNCCCAGCGCCGCGCGGCCACTTGGATGCGACCCGTTTCAAGTCCCTTCATCAT  
CTGCGAAAAGCCTTGACCCATGGCTCCGCCCAGGATCGCCGAGACCGGCACCCGGAGGTTGTCGAACGACAGCTCGCA  
GGATTTCGACGCCCTTGTAACCCAACCTTCGGCAAGTCCCGGACACCGTGAGTCCCGGCCCGGTTTCGACGAGCAGCAT  
CGACATGCCTTGGTGCCGCGGTGTGGCGTTCGGGTCGG

## Clone Rv32

:::Rv32SP6.seq:::

GGCATACCAATGTGGACTTCTGCTCACCACGATATCCGTGGTCTGATCCGCTGCTGCGGCGGGCTGCNACCTGCNTC  
TCNCGCGCACCCGTNACTACATGGCNCGCGCCGACGCATACGTGCGGCGGGACCCACTCCNACTGGTTCGACGGTGC  
TGGCCGCGTGTCCGCANGTCCCNAAACCCGCGCCGACCGACGAAACCGGCGCCGTCCGTTCTGGACCAACGCTCATGT  
GCCGTGCGGGTCCATGCTCGACGCCATCGAGACCGTAACCAGCGTCTCGAGCGGTTCCGCTCCGGCTTCCGTGACAT  
CTTCGTGGCTGCTCGCGCCGTGCCGCCGCGGGATGGTTCGACCACAACGCCAACACCTCGGCGGTGACATCACCGTC  
CGCGCCACTCGACCTGGCGCGCGATCGCGGCC

:::Rv32T7.seq:::

GTGAGCAGACCTACGCCNCCTGGTTGCGCCAACCTCGGTACCGATCATGGCGCGCNGCCTGTCTGTCACCGATACCCAGC  
GAACAAGACAGCCCGGTCCGCGACAAGATGACTTTCGGGATCTCTTCGGCGACTTCCATGGGGTTCGTCCGGAGTCCCG  
GGCGCCACCGCGAGGTAACCTCTGTCTCAGTCCCATACGCGACCGGGTATCCACGTGCGGCAACAACGCCACACCTC  
CCCAGACGCCNCCTGTACGCGGTGGGTTCCACNGCAATAAGTGGCCTCANGGCATCGTCCGGCGGCGGTCCNCAAC  
GCA

## Clone Rv330

:::Rv330SP6.seq:::

CTCAAGCTTGAGGTTAACTTTGAACGGATCGAGCTGGACGTTTCGAGACGGTGATCGGGCCGAACCTGAATTGTCCGGT  
AATGCCCAACGCAAAAAGCAGGGTGGTGGCCGGGGCGGTGAAACCGCGCTCGGCGGCACCGTCGAAATCTATGTGGAT  
TGCCGGAATGGGGATGTCCGGCACGGCGAAACCGTAGTTCGCTTGTCCCGTGAGGCCAGGTGGATGGGGGAAAGAT  
CCTGGTGTCCGGGATAATAATGGGGCCGATGCCGCCGGTTGAAGTCCACTGGATCGGGAATTCCGGAATCTTGATCCG  
ACGTTTCAGGCCGAACAGGCCCTC

:::Rv330T7.seq:::

CGGCGACGTGCGGATACGCCGAGCAGTTGGGAATCGCTCTGCAGCAAACCAATATTCTGCGCGACGTTTCGAGAGGACT  
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CACTCGATGACCCCGACGGACGGCTCGCGGCNCTGCTGCGGTTTCAGTGCCGACCGCGCCGCGAGACTGGTNTTCGTGG  
GACTGCGGCTGATTCCACACCTCGACCGCCGACGCGTGCCTGCTGTGCGGCCATGTCTGGCATCTACCGCCGTCAGC  
TCGCCTTGATCAGAGCATCGCCGGCGGTCTGCTA

## Clone Rv331

:::Rv331SP6.seq:::

CTATAAAATACTCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACCACGCGCGGGTTCGGGCGCCG  
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CCGGGCGGAGCTACATCGGCTCGGCCGCCAGTGTTCCGGGCCCTCTTCGAGGTCNAGGTCNATACCGATTTCGCGCAT  
CCGCAGCCGACCCCTGAACNACANAACCGTGCCCTACTATTGCTTGTGTCGCGGGGCCAAAAACAGCTTGGCATCCT  
GGCCCNATTGGCCGGCGCGG

:::Rv331T7.seq:::

CTTCGGTTCGAGTGTCGAGTGATAGATGACGACCGGGACCTCGTCGGCATCTTCCATAGCCCGCCACACCTTCAGTT  
GCTCACCGGAATCCAACCGGTAGAAGGTGCGCGAGCGCTCGGCATTGGTCATCGGGATATGCCGCTCGGGACGGTCAG  
AGCCCTCGGGTCCGGCCAGCACTCCGCAGGCTTCGTGCGGGTGGTCGCGACGCGCATGGGCCACCATCGCATTCACCA  
GGTCTGCGGAATCNCCANACGTANACNGTTCCTTTCTAA

## Clone Rv333

:::Rv333SP6.seq:::

CTGGCACCAAGGCCCCACACGTACCCCTGTGACCTCCTGCGCCGACCCCGCCGAGGTCCTGGCCGTTACCACCGAAC  
GGGCGAGCCGGGAGTCTGGTNCGCATCGAACAANAGCAAGGTGCATGGGCGGAGTTGTTCCGCCACTTCGTTCGATGA  
CGGGGTCNATCCATTTCGAGGTCCGTCGCCGCGTCCGTTCNAGTGGCGGTTCACACTCCAGGTAATCGACCTCACAGACNA  
AAGGACTCNATCCCATCTAGGTGTGGACNAAACAGATCTTCTGTCCGACNACTACACCACCACCCAGGCCATCGCCGC  
CGCCCGCGATGCCAACTTCGACGCGGTACTGGCCCCGCGGGGGGCGCTCCCCGTTGTCAACACTTGCCGTGTTCTNT  
TCACGCNCTGCCCCACATCCAACCCCAACG

## Clone Rv334

:::Rv334T7.seq:::

GTTCTTGGGCCCATGCGGAGGTATCGCCGTTTCACCCACGCGGTTCGGGGTGGCGTTGCATTAGCTCACCGATGGTGCG  
CTTGTGACGGCCCGGGATACCCGAGTGCCCGTAAACCATCTTGTGCTGC

## Clone Rv335

:::Rv335SP6.seq:::

CAATACTCAAGCTTGGCGTGCCGTTCCAACCCGAATTGGCTTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTCA  
ACNACNACGTCGTCCGCGGGACACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTAC  
AACGCCGCGCGGAACGCTTCCGCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATC

:::Rv335T7.seq:::

CNTCATGATGATCATCACCCGAAGTGTGGTAGCCGAGTGGTTATCGTGGGTACCGTCGTGCTTTCCATGGGCGCCTC  
TTTCGGGCTTTCCGTATTGGTCTGGCAGGACATTCTGGGTATCGAGTTGTACTGGATGGTGTGGCGATGTCGGTGAT  
CCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCCGGTTGAAAGAGGAAATTGGGGCCGGATTGAA  
CACCGGAATTATCCGTGCCATGGCTGGTACCGGGGAGTGGTGACGGCTGCCGGCATGGTGTTCGCCGTTACCATGTC  
GTTGTTGTGTTAGCGATTTGCGAATTATTGGTCAGATCGGTACCAC

## Clone Rv336

:::Rv336SP6.seq:::

ATACTCAAGCTTTTACGGTGATCGCNCATCACCTGGTTCATGAAC TGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCA  
ACATGAGCCAGCCTCTCGTCGGCGGTTCGGGTGCAGGTGCTCGGGCAGCTCGGCCGCNACAGCCGCCTGACCCTGAAAC  
CAGCTTCCATATCCCGCGANNAACGACGCCAGTCCGCTACGTNACCCCTCCGCGACTGTCCATGGACAACAGCGCGTT  
CTCACCGACCGGGCCCGGTGTGGGGTNTT

:::Rv336T7.seq:::

GCTGGTAGAGTCGCTGACCGGTGCAGTTTCGACAATGTGGTGCCGGTTCGGCGGCTACGTGCCATCGAGACACTGGC  
GCAGGCTATCGCACCCGTTATCGGCTACGAGCAAATCGCGGTATGCGTTCTTGAGCATGAGTCGGCGACCGTCGTCAT  
GGTCGACACCCACGACGGAAGACGCAGATCGCCGTCAAGCATGTGTGCCGCGGATTATCAGGACTGACCTCCTGGCT  
GACCGGCATGTTTGGTCGCGATGCCTGGCG

## Clone Rv337

:::Rv337SP6.seq:::

GCTTTCCGCCGATACCCGCCATGTNCGCACATCCAGGACTTCTGGGGGGATCCGCTGACAGCGGCGGGATCCCAAAG  
TGCGGATGATCGGGCCGCCTACGTCGTGGTGTACCTCGTCGGTAACAACGAAACCGAAGCGTATGACTCGGTCCACGC  
GGTGCGGCACATGGTGGACACACACCGCCACCGCACGGGGTGAAGGCTATGTACCGGTCCGGCANCACTCAATGC  
CGACCCAGGCCGAGGCCGGANACAAAANTATCGCTAAGGTACC CGCATCACNAGCATGGTGATCGCAGCAATGTTGCT  
AGTGATCTATCGCTCCGTAATTA

:::Rv337T7.seq:::

CTTCCAACCCGAATTGGCTTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTCAACGACGACGTCGTCCGCGGGAC  
ACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGCTTCCG  
CCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCGGAGCGACGGC  
CAAGSGCGGTGCCANTGTCGCCCCGGGCGCACGGTGCGGACAAGGTGGTGCTGGCGGTCCCGATCGGCCCA

## Clone Rv338

:::Rv338SP6.seq:::

TACTCAAGCTTCGCGAGATCCGGATGGCACTCACGCTGGACAAGACCTTCACAAAATCTGAAATCCTGACCCGATACT  
TGAACCTGGTCTCGTTCGGCAATAACTCGTTCGGCGTGCAGGACGCGGCGCAAACGTNCTTCGGCATCAACGCGTCCG  
ANCTGAATTGGCAGCAAGCGGCGCTGCTGGCCGGCATGGTGCAATCNACCAGCACGCTCAACCCGTA

:::Rv338T7.seq:::

CCCACGACTTCTCTCTCGATCAGTTGGATTTGTACGAAGAGGCAACGAAAGCAGTGATCCTCGGGATGGTCGACGCCCT  
ACATCGACCCGCCGTTACGCGCCGACAGCCTGCTAGATGCGCTGGGCGAGCAGGTCCACAGTTCGCCGCTAAGGCAC  
GGGTCGTGTTCCCGTCCGGATCGCCATTGCGGCTCGGCGTCTGCTCCATTGATCAATAGGGCTGGCAGCTCCGTC  
GGCAGGGGCTACGCTCACCCGTCACG

## Clone Rv339

:::Rv339SP6.seq:::

CTCAAGCTTATGCGCGCCGGCCGAGGTCTGCTCACGGCAACCCCTGAAGTTTAGGGGACNACCTACTCAGCGCAAAAT  
TTCCGCTAATGTGAGTCCGCCCCACAGGGGNNATCAACCCATGTGATCATGATCTACCCGGATACCGGATTGGCGG  
TAGCGCCCAACGATCGTCNAAATNTCCGCTGAATCATCGGATAGCTCCGGCGTCAACGCGTTTTGANTTCACCGC  
GCAACAGCCGCCAGGCCGGCCCGCANCGANCCGATCTCNTCGGGCCGCATGGGCCCAATCTTNTCG



## Clone Rv344

.....Rv344SP6.seq:.....  
TCAAGCTTTAGCTGCCCCGAATCCGTACNCCCGATGCNCCCAGATCGGGGCTTCGCANATAAAGCACNAACAGGCGGGC  
AAAACGTCNATCTCGGAGCCGGAAGGGCAATCANCCGACCGTCNACAAACGACACCGGCGANACCACTTAGGCAGTGA  
CGGCCGGCCCCGAACATTACNCGCTCGTTGATTAGGCGTTTCGGTCTCGTCCGCGGTCATGCCGAGCAGCTTTCGGGCANA  
TCTGAACGCTGTCTGTCCGGGAGCGGCGCCGGGCGTTGGGGTGCCTGCGGAATGTGACNAAACGAGCCGGACCCN  
TCTCGGCG

.....Rv344T7.seq:.....  
CCGGGGCCACTCCGCACAATCNGTACCNNACCAANATCTACACCATCGAATACGACGGCGTCGCCGANTTTCCGCGGT  
ACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTTTCATCCTGACGC  
CGGAACAAATNGACGCNTCGGTTCCGCTGACCAATACGGTCGGTCCC

## Clone Rv346

.....Rv346SP6.seq:.....  
NCTGGCCTTTGGTCCACACTAANACAATACTCAAGCTTCCGGCCGAGAGCCGCCAACTCACGATATCGTTAACCGAT  
ATCCCAGCCGATAGCTGGCGGGCTCGGGTGGTGGCCAGCGGCTGCGACNAAAGGTGTGACCGTCATGAAACAGAC  
ACCACCGGCGGCGCTCGGCCGTGCTCACCTGCTCGANATCTCAGCATCCGACGCGGTTGTATCGCGCTTTTCGGCGTG  
TNGTGGGTCNCCGCCCGAGCCCGGCAAGGCCGGCCGACACAACCCCGGAAC

.....Rv346T7.seq:.....  
CATCTGCCCACCACACGGACCGCGGTGCGGACGCGGCTGACGCGCCTGGTGGTCAGCATCGTGGCCGGTCTGCTGTTG  
TATGCCAGCTTCCC GCCCGCAACTGCTGGTGGGCGGCGGTGGTTGCGCTCGCATTGCTGGCCTGGGTGCTGACCCAC  
CGCGGACGACACCGGTGGGTGGGCTGGGCTACGGCCTGCTATTTCGGCTGGTGTCTACGTCTCGTTGTTGCCGTGG  
ATCGGCGAGCTGGTGGGCCCCGGGCCCTGGTTGGCACT

## Clone Rv347

.....Rv347SP6.seq:.....  
GACAATACTCAAGCTTGACTGGCCACCCACCGGCATGACCACCGACAGGCCCGACTGGTTCGTACCACTCGAACGCCGG  
GGTGTGTGATGTCCCAGCCGCTGAANTCGTCCTGCGCGCGCAGGCCGTCNAACAGGTACAGGGCGGGCGAATTGGCACC  
ACCACTTTGGAATTGGACCTTGATGTACGGCCCATCGACGGCGACGGCACCTGCAGGTACTCCACCGGCAAGCCCGG  
CCGGGAAAATGCCCCCGCGGTCNCCGTGCCACCGACGGCGCCGANCAAACCCGACACTAGGGCCGCGCCNACGGCCCC  
GACCACNANTCNACGCGACATACCCGTGACGGCGCCACNAACCTGTCAACA

.....Rv347T7.seq:.....  
CCTCCAACCTCGGCGGGGAAGCGACNCCAGCCTACCGAGCTTGAGTCCANGACGCCAGCGGCGGGCGTGGTCTGCGTC  
GTGGTGCCGCGGGGTGGCGTTGGCTGGCAACGATCTCCACCCAGCCGCTCGGGTTACCCACGATCTCGGCATANACG  
CGGGCCGAGGCGGTTGCGATAACCGTATTGCGTCAATTGGGACGCGGTTGTGCATTTCGGCTAGCTCGGTTGCCACACCC  
GTCAGGGGTTTCGACGTTGGCGGGTTTCGGCGGGCCCCANACCGCTGTCAACCATGCCCCGCAAGCCGACCTGCGGCGCC  
ACCAACTGCAGCACCANCATGTGCGCGTCGCGCGCCGATCAGATGG

## Clone Rv348

.....Rv348SP6.seq:.....  
CTCAAGCTTTTTGAGCGTCGCGCGGGGCANCTTCGCCGGCAATTCTACTANCGAGAANTCTGGCCCGATACGGATCTG  
ACCGAANTCGCTGCGGTGCANCCACCCTCATTTGGCGATGGCGCCGACNATGGCGCCTGGACCGATCTTGTGCCGCTT  
GCCGACGGCGACGCGGTAGGTGGTCAAGTCCGGTCTACGCTTGGGCTTTTCGGACGGTCCCGACGCTGGTTCGCGGTT  
GCGCCGCAAAAGCGGCGGGTTCGGGTGCCATCAGGAATGCCTCNCCGCCGCGGCACTGCACGGCCAGTGCCGCGGCGA

.....Rv348T7.seq:.....  
CNCCAGCTTGATTGGTCTGGTTGCATTGGCCAGCTGCGCGAGCCTGGCTCACTTCAACTACGACGACCGCAAACAATT  
GCCGCTTCGGATCCGAGTTTCGGTTGGGTACGCGGCAATGGAGCACCATTTCTCGGTGAATCAGACTATTCCTGAGTA  
CTTGATCATCCACTCTGCACACGACCTGCGAACCCCGCGCGGCTTTCGCGACCTGGAGCAGCTGGCGCAACGTGTGAG  
CCAGATCCCAGGCGTTGCCATGGTTTCGCGGTGTGACCCGGCCAAACGGGGAAAC

## Clone Rv349

.....Rv349SP6.seq:.....  
CAATACTCAAGCTTGACTGGGCCCCGACCTTCGGCGCCACCCACACCGTCAACGCCCCGGAAGTCNACGTCGTCCAGG  
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CCTTCTACGCCCGGATCTCGCCGGAACCGTTGTGCTGGTGGGTGTTCCNACGCCCGACATGCGCCTGGACATGCCGC  
TGGTCNACTTCTTCTCTCACGG

::::::::::Rv349T7.seq::::::::::

TCGACGGTTTGGCGGCCTTAAATGCACTGAGGTCGTCAATTGACCCACAGCGGAAATGCCGACTATTTCGAGGCCTC  
CTTCGCCTTGGCTGCCGGAGAGGGGCTCCGCGGAACCGCATGCAGGTATATGACCTCGGTTTCTCGGGTGCTACCGC  
GTGCCTTGTNTANGATNANCTCGGCGTTGGAATTGTCCAGCCGGCCCAATTTCATCGAGCGCANATTCGTACACNTGGC  
CGGCGGCGACATACGCTTACCGTGGATCTGCTCCACACGGACCGCCCTGTCTGGGATCCTGCTCACGGGTAANGGAAC  
TTACGTGGCACTCGG

Clone Rv34

::::::::::Rv34SP6.seq::::::::::

GACCACGCCAGGCTAATCACGTGACGCTACCGAATACCCTNCCTAGTGGTGCAGGCTCCCCTGGAAATGGCCCTGTA  
CCAATCGCGCACCGGTGCCAG

::::::::::Rv34T7.seq::::::::::

CGGCACCCGACCCCTTTGAGCCGTCCGCCGTGGCCGGTGGAACTGGCCGACGAGGGACTGATCGTGCTGGGCAAAT  
TGGTCGATGGCACGCTGGCCGCCGATCTGAAGGTCN

Clone Rv350

::::::::::Rv350SP6.seq::::::::::

CTCAAGCTTGCCGTTACCCCGACTTCCGGAGGGACACCATGAGCACCGCCAGCCGAGCACGAGGGCCAAACTCCGCCGA  
CGCAGGCCGGTTGGACTTGTCTGCTGGACAAGGGGTTTAGCCGCCGAAGCAGTGACGTACATCGGCGAAAAGCAGTT  
CGCCTGTTCGACCGACGNGCANNACCGTGAGGCTAGGGAAGCGAGGAGCACATGGCCGCCGACCCGCAATGTACACGCT  
GCAAGCAAACCATCGAACC CGATGGCTATNCNTCACCGCCCATCGCCGCGGT

::::::::::Rv350T7.seq::::::::::

CATGTCGCGCACATCCAGGACTTCTGGGGGGATCCGCTGACAGCGGCGGGATCCCAAAGTGCGGATGATCGGGCCGCC  
TACGTCGTGGTGTAACCTCGTCGGTAACAACGAAACCGAAGCGTATGACTCGGTCCACGCGGTGCGGCACATGGTGGAC  
ACCACACCGCCACCGCACGGGGTGAAGGCCTATGTACCGGTCCGGCAGCACTCAATGCCGACCAGGCCGAGGCCGGA  
GACAAAAGTATCGCTAAGGTCAACCGCATCACGAGCATGGTGATCGCAGCAATG

Clone Rv351

::::::::::Rv351SP6.seq::::::::::

ATACTCAAGCTTCGGTACGGTGGCGGGCCGTGCTGCTGGCCGCGGTGCGGGCGTGCAGGCTGCGGTCTCGTTTACN  
AGCTCGCGCTGCTGACACTGGCGGCNAGCCTGAACGGCGCGGGGATCGTGGCCACCTCCCTGATCGTCGCGGGCTACA  
TAGCCGCGCTGGGAGCAGGCGCCTTGCTGATCAAGCCGCTACTTGACACGCGGCCATCGCGTTCATCGCCGTGGAGG  
CGGTGCTGGGCATCATCGGCG

::::::::::Rv351T7.seq::::::::::

TGTCAAGTCCTTTTCAATCTCNTTTTATGACATGACTGGAGATCTGTCTAGATTGCAGCTCCTGTGAGCGTGGGTAC  
CGGATTCAGCCGGTTCGGTACGCCCGGTTGGTACCGGCTTTGCGGCAGTGCTCGGCCTCGAGTTTCGGCGATCGCGCG  
CGAAGTGCGTTTCGCGCAGCAAGATCGCGGCCGTAATGCCGCGGATGACCGCGATGACCAGCGGATCCAGGAGAACCG  
TTCCAACCAAGTGCTGGGCGGCCATCCCGCGGAAGTAGACCAGTGCAAGTGGTGCC

Clone Rv352

::::::::::Rv352SP6.seq::::::::::

CAATACTCAAGCTTCAAAACAGGCCTGTTGTGGGCGCACCCGGCTCGCCGAGTTCTGCACGCACCGCCTCAANTGCGG  
CCCGCACCGCCGCGATCTCCGGTACGCAGGGCCGCGGCCGCCGACGNGTGTTTCGCGCAGTTTCGCCGT  
CAATGATGCTGACCTGATCGGCCACCCGGGCGTTCTCGGCGTCGTCNCGTTCACTAATCGCGGTGCTC

::::::::::Rv352T7.seq::::::::::

TACGCTGGCGCTGGAGGGAGCCANNTACAACATCCACGCCAATGCTCTTGCCCCGATCGCGGCGACCAGGATGACCCA  
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GGAGTGTCGCGACAACGCATCGGTGTACGTCGTCGGTGGTGGCAAGGTGCAGCGAGTTGCGCTGTTTGGCAACGACGG  
CGCCAACTTCGACAAACCGCCGTCGGTACAAGATGTTGCGGCGCGGTGGGCCGAGATCACCGATCTGTCCGGTGCGAA  
AATTGCTG

## Clone Rv353

:::Rv353SP6.seq:::

GCTTTTCCCGTCCGTCNNCGCTCAACCGCGTGAGGCCGAAGCGGNTGGTTACGACTCCCTGTTTGTGATGGACCACTT  
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GACCGANCGGCTGCNNNTGGCGCGTGTGGTGACCGGCAATACCTACCGCAGCCCGACCCCTGCTGGCAAANATCATCAC  
CACGCTCGACGTGGTTAGCGCCGGTCGAGCGATCCTCGGCATTGGAGCCGGTTGGTTTGANCTGGAACA

:::Rv353T7.seq:::

CNGCTTTTAAATGGCCTTGACNTGGGCGNGCCGGCCACCGGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTAC  
ACCATCGAATACGACGGCGTCGCCGACTTTCGCGGTTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGC  
ACCTACTAGTGCACCTCAACTACTTCATCCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTC  
GGTCCACGATGACCCAGTACTACATCATTCGACGCGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATC  
GTGGGGAACCCACTGGCGAACCTGGTTCAACCAAACTTGAAGGTGATTGTTAACCTGGGCTACGGCGACCCGGCCTAT  
G

## Clone Rv354

:::Rv354SP6.seq:::

CTCAAGCTTGCCGGGAGGGTGCATGGCCGACTCGGATTTACCCACCANGGGGCGCAACGCGGTGTCCGCGCCGTCNA  
GCTGAACGTTGCTGCCCGCTGGAGAACCTGGCGCTGCTGCGCACCCCTGGTCGGCGCCATCGGCACCTTCGAGGACCT  
GGATTTTCGACGCCGTGGCCGACCTGAGGTTGGCGGTGGACGAGGTGTGACCCCGGTTGATTGCTCGGCCCTTGCCGGA  
TGCCACCCTGCGCCTGGTGGTCGATCCGCGAAAANACGAANTTGTGGTGGAGGCTTCTGCTGCTGCGACACCCACNA  
CGTGGTGGCACCGGGCAGCTTTAGCTGGCAT

:::Rv354T7.seq:::

CCGACGCCGTCGTGGCCACCAACACCGCGACCGAGCACCGTGACCCGGACCGGGGTGCCGCGGAACCGGTCTTGCCCA  
ATTGCCGCGGCACCAAGCCGTCGCGCGCCATGGCGAACAGCACGCGGCATTGCCCGAGCATCAACACCATCACCACCG  
TGTAAGCCCGGCCAGCGCGCCGACGGAGATGATGCCGCTGGCCAGTACACCCCGTTGGCCTGGAACGCGGTGGCCA  
GATTTGCCGGCCCGCGGCCCGGTACGGTCCGCAGTTGGGTGTATGGAACCATGCCCGACAGCACCCACCG

## Clone Rv355

:::Rv355SP6.seq:::

TTNACTGGCCTTTGGTCCACACTAGACAATACTCAAGCTTCCAGGACATCGTCATCGCGACCAAAACCGCGAGCTAGG  
TCGGCATCCGGGAAGCATCGCGACACCGTGGCGCGAGCGCCGCTGCCGGCAGGCCGATTAGGCGGGCAAATTAGCCC  
GCCGCGGCTCCCGGCTCCGANTACGGCGCCCCGAATGGCGTCACCGGCTGGTAACCACGCTTGCGCGCCTGGGCGGCG  
GCCTGCCGGATCAGGTGGTAAATGCCGACA

:::Rv355T7.seq:::

NGACGTCTTCCATCCGCGCGTCGTTTGGCGGGTTGGCCACAGCAGCCCGCCGGTGACGGCGACGATGCTGGGCTGGT  
TGCGGCCCTGCGCCACCGCGGCTTGCATGCTGGTTGGCTGTCTTGGGACGATCCCGAAATAGTCCACGCGGATCTGGT  
GATTTTGCGGGCTACCCGCGATTACCCGCGCGGCTCGACGAGTTTTTGGCCTGGACTACCCGCGTGGCCAATCTGCT  
GAACCTCGCGGCCGGTGGTGGCCTGGAATGTCGAGCGCCGTTACCTA

## Clone Rv356

:::Rv356SP6.seq:::

CTTCCTCCTGAGTACNCCCGTNTACTTTGGGATGGGTAAAAAGGCGAATCNCCGTTTGGTCACGAACGCCGGGAGGG  
ACAATCTCGGGCGGCTGGGGCCTCTCGCGGGAANGCCCGAATGTACGGTGTCTCGACACTTCCCNCCCCCTCCG

:::Rv356T7.seq:::

GAGCATCGGGACNTACGGAGTCAACTACCCGGCCAACGGTGATTTCTTGGCCGCGGCTGACGGCGCGAACGACGCCNG  
CGACCACATTACGAGATGGCCAGCGCGTGCCGGGCCACGAGGTTGGTGCTCGGCGGCTACTCCAGGGTGCGGCCNT  
GATCNACATCGTCACCGCGCACCACTGCCCGGCCCTCGGGTTACGCGAGCCGTTGCCGCCNCAGCGGACGATCACNT  
CGCCGCGATCGCC

## Clone Rv357

:::Rv357SP6.seq:::

TACTCATGANCATCCTTTAATCANNGCTTTGCGTTTTTTTATTAAATCTTGCAATTTACTGCAAAGCAACAACAAAAT  
CGCAAAGTCATCAAAAACCGCAAAGTTGTTTAAAATAAGAGCANCACTACAAAAGGAGATAAGAAGAGCACATACCT



## Clone Rv361

.....Rv361SP6.seq:.....  
GCTTGC GG GTGATCGCCTTGGTCAACGGCACC GTGATCGGATCGGGGTCNACCGCNCAGATGGACTGGANCTTCGGCG  
AANTCNTCGCCTATGCCTCGCGGGGGGTGACCCTGACCCCGGGTGACNTGTTCGGCTCGGGCACGGTGCCACCTGCA  
CGCTCGTCAAGCACCTCNGGCCACC GGAATCATTC CCGGGCTGGCTGCACNACGGCGACNTGGTCNCCCTCCAGGTG  
AAGGGCTGGGCNAAACAANGCAGACCGTCCGGACAANC GGCACTCCTTTCCGTTGGCTCTTCGGCCGAATCCGGACG  
CCNAACCCGACCGCG

## .....Rv361T7.seq:.....

GTTCTCGCAGATTTCCGGATTAGCGGGACTGGTCACCAGTTGGGTATGCGGGAAGGCGCTGACGTTCCGCCGCGATTA  
GCTGTTTGATGGACGCGGTGGTGATGTNCTGATCACGGAACTGGCTGTAATANCC CAGGGTCGCCNCGCTTTTCATCCG  
GGCCCCGACCCGGCGCACCGAGCGTGTGCGCGAGGTATGCGACGTGATTTTCGCTGAAGTCCCCGTACCCGGAGAACT  
CGAACACGCTGAGGCGCTCGTCACCGTCGTNNCGGCGACCAAGCGCGGCGAGCAACTGCGCAAAATCGTTAAGANAGG  
TCGAATCGTTGAAATTCGGCACCACTGCACC

## Clone Rv363

.....Rv363SP6.seq:.....  
CACAAACAATACTCAAGCTTCAGGTCAATGTGCNCCAAGCCCTGACGCTGGCCGACCAGGCCACCGCCGCCGGANAC  
GCTGCCAAGGCCACCGAATAACAACGCCCGCGAGGCGTTCGACGCCAGCTGGTGACCGCCGAGCANANCGTCNAA  
AACCTCAAGACGCTGCATGACCAGGCGCTTANCGCCNCAGCTCAGGCCAAGAAGGCCGTGCAACGAAATGCGATGGTG  
CTGCAGCANAANATCGCCGANCGAACCAAGCTGCTCAGCCAGCTCGAGCAG

## .....Rv363T7.seq:.....

CCACCCGTGCATGGTGGCACTGTAGCGACGTGCTGCAATCAAGGTGATGCCCCGACTCTGGTCAGCTCGGAGCCGCTGA  
CACCCCGCTAAGGCTGCTCAGCTCGGTGCATTACCTCACCAGCGGCGAACTCCCCAGCTTTACGACTATCCGGATGA  
CGGCACCTGGTTGCGGGCGAACTTCATCAGCAGCTTGACGGCGGCGCTACCGTCGATGGCACCAGCGGGGCGATGGC  
CGGGCCCGGCGACCGATTCTGCTTCAACCTGTTGCGTGAACCTTGCC

## Clone Rv364

.....Rv364SP6.seq:.....  
GCTTTCGCCGATACCCNCCATGTCCCGCACATCCAGGACTTCTGGGGGGATCCGCTGACAGCGGCGGGATCCCAAAG  
TGCGGATGATCGGGCCGCTACGTCGTGGTGACCTCGNCGGTAACAACGAAACCGAANC GTATGACTCNGTCCACGC  
GGTG

## .....Rv364T7.seq:.....

CAACCCGANTTGGCTTTCGGCGCCNTCGGTGAGGACGGCGTGCGGGTGCTCAACGACGACGTGTCGCGGGGACACAC  
CTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGATCTACNACGCCGNGGGAACGCTTCNGCCGC  
GGGCGTGACCGCNTCCCGTT

## Clone Rv365

.....Rv365SP6.seq:.....  
GGGATGGGCAAAAAGGCGAAGCACCGCTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGGCTAGGGCTTCTCGCG  
GGAAGGCCCCGAACGTACGGCGTTTCAACACGTGCGCTGCGCCTCCGACCGCGAACATTGCGGGATGGCAGCAACCTGG  
TAGCACCTGGCCGGGCGATGATCTGCCAGCGTCCCCGCGGGTAGTCGCCGCCCCGGCGG

## .....Rv365T7.seq:.....

CAGCAGACCAACAAGAGCATCGGGACATACGGAGTCAACTACCCGGCCAACGGTGATTTCTTGCCGCGCGTGACGGC  
GCGAACGACGCCAGCGACCACATTCAGCAGATGGCCAGCGCGTGCCGGGCCACGAGGTTGGTGCTCGGCGGCTACTCC  
CACGGTT

## Clone Rv366

.....Rv366SP6.seq:.....  
CTCAAGCTTGACTGGCCACCCACCGGCATGACCACCGACAGGCCCCGACTGGTCGTACCACTCGAACGCCGGGGTGTTT  
GA

## .....Rv366T7.seq:.....

TTGGTGCCCGGAATGGCGAGTCCCATTANTCGCTGATTTGTTTGAACAGCGACGAAACCGGTGTTGAAAATGTCGCC  
TGGGTGCGGGATTCCCTCTCCAAGCAAGAGTAACTGGCCCCAAATAAAGTTACTCGTCGTCTTGCAAAGACCGCTACC

CGATGCCATTTATGTGTTTCCTTACGCTCNNTTCCGGTGCGCCATCATTATCTGCACCTTTGCACTGCACATTGAG  
CTTAGCAGCGCTCG

## Clone Rv367

.....Rv367T7.seq:.....  
GAATTNGCTTTCGGCGCCATCGGCCCAGGACCGGTGCGGGTGCTCAACGACGACGTCGTCCGCGGGACACACCTCGA  
TGCTGCCGCCATGACGCGGTGGAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGCTTCCGCCGCGGGCG  
TGACCGCATCCCGTTGACCGGGCGGATCGCNGTGATCGTCGATGACGGCATCGCCACCGGAGCGACGGCCAAGGCGGC  
GTGCCAGGTCGCCCCGGGCGCACGGTGCGGACAAGGTGGTGCTGGCGGTCCCGATCGGCCAGACGACATCGTGCGGAG  
ATTGCGCGGGTACGCCGATGAAGTGGTGT

## Clone Rv368

.....Rv368SP6.seq:.....  
TAAAGCTTTCGTCACTTCATNGNGCCCCCGGACCAACAAAAGCATCGGGACATACGGAGTCAACTACCGGCCAACGG  
TGATTTCTTGGCCGCCGTGACGGCGCNAACGACGCCAGCGACCACATTGAGCAGATGGCCAGCGCGTGCCGGGCCAC  
GAGGTTGGTGCTCGGCGGCTACTCCCAGGGTGCGGCCGTGATCNACATCGTCACCGCCGCACCACTGCCCGGCCCTCGG  
GTTACGCGAGCCGTTGCCGCCCGCAGCGGACGATCACNTCGCCGCGATCGCCCTGTTGCGGAATCCCTCGGGCCGCGC  
TGGCGGGCTGATGAGCGCCCTGACCCCTCAATTGGGTCCAANACCATCNACCTCTGCAACAACGGCGACCCGATTG  
TTCGGACGGCAACCGGTGGCGANCGACCT

.....Rv368T7.seq:.....  
CCGGGAGGGACCATCNCGGCGGCTNCGGCTTCTCTCCGGAAGGTTCTANNGTNNNGCGTTTCNACNCTTCCCGTCGC  
CCTGCGACCGCCGAACATTGCGGGTATGGNNGCANCTGTNAGCATCCNGGCCGGGC

## Clone Rv369

.....Rv369SP6.seq:.....  
CTCAAGCTTCCGCATCAGATCGCTATAGAACCAGTGCGCGTCCCCACCGAGTGGCTGGTGCCTTCCAGCACGATCGT  
TACCGCGTTATCGGAATCAAACCTCNCCGAACACCTGACCAACGCGCTTGATCGCCTGAATCGATGCGGCGTCGCTGGG  
GCTCATCGATACCGAGTGTGCTTTTCCGACCACTTCCAGTTGCGGTACGGCGAGATTGACAAAGGCGGTGAAGCCCAG  
CCAGAGCAGGACGATCACCNCCGCAAACCGGCGGATTGCCCCG

.....Rv369T7.seq:.....  
GCTTGGCAGCCTGCGGCTGGGCGCCCTNGAGCTCTTCGATCTGGATCTCCGGACTCGAGATGCTCACTTGCCCGGCCG  
TGGACGTACCCATTGCGGCCGGGACCCAGCGCCCCAGGTGACCAGCGAGTTGGGCTGCACGCTGACCGGCCCGTCGG  
GGTCGACGCCGGTAACGGTCAGCAGCTCCGANGTCCNNTGATCCCCGACCGCAGCTGCCAATGCGCGGCTGGCAGCCG  
ACGTGGATGTGCCGGGGCTAGATCGCGGGGCGAGCGAGACCGCGTCACCGACGGTCATCACCTTGCCGAGTTTNG  
GCCTGCCGCAN

## Clone Rv36

.....Rv36SP6.seq:.....  
GCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTNCACACAGGAAACAGCTATGACCATGATTACGC  
CAAGCTATCTAGGTGACACTATAGAATACTCAAGCTTGAGCCATCGGGCTATCAGCTGGTTGATGTCCCG

.....Rv36T7.seq:.....  
CAGGCATGCAAGCTTGTGCTCTATCACATCCGACCACCAACCGCCCCGACGGCTCGGCAGAACGCCTCCGCATATGGGT  
CGACGACCAGCGGGTCGGACTTCTGGGCTGCCAGCGCTCGCGCCGTGCGGACAAACAGCGCGGTGGAACCGACACTCC  
TTGTGATGTCCACCTATCACCTTCGGTACGCACCAATCGACCCTACGCGGCTAGCTCAGCCCCGATCTTCCAGAGC  
TCCGCCCG

## Clone Rv370

.....Rv370SP6.seq:.....  
GCTTTTTGAGCGTCGCGCGGGGCGGCTTCCCCGGCAATTCTACTAGCGAGAAGTCTGGCCCCGATACGGATCTGACCGA  
AGTCGCTGCGGTGACGCCACCCTCATTGGCGATGGCGCCGACNATGGCGCCTGGACCGATCTTGTGCCGCTTGCCGA  
CGGCGACGCGGTAGGTGGTCAATTCCGGTCTACGCTTGGGCCTTTGCGGACGGTCCCGACGCTGGTCGCGGTTG



## Clone Rv376

.....Rv376SP6.seq:.....  
GCCANCCGGCTTGGCGTCGACTCCCGTTCNGCACATCATACGGTCCCCGGTACTGTCCAACGCGCCGGTGGCTAGC  
CAAACGTCACGACTCTCAGTGATCCCAGTTCGTGATCCGGCCGGTGGCGCCGCTGCGGCGGGGGCTNATNTACTTCGG  
ACTNATTATCTCATCAAAGGACACCGGGCCGGTGGCTGGAATCCCATGGTGGGATCGGCCACACAN

.....Rv376T7.seq:.....  
CCGACCTGGTATCTTCCGATAGCGCGCTTGATATCCGGTCTGATCTCCTGCCCTTAACGCCGGATCTCAGCAGGTCC  
CCATGCAAAGATCCGAGGTGTCCNGATCTAGGGGTCTCGTCCCTCCAGATGATGGAGCAAGTCGGCCC

## Clone Rv377

.....Rv377SP6.seq:.....  
CTCAAGCTTCCGCTCAGGCGGCGCTGCCGGTAACGTGCGTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTCGGC  
GGCTACGTGCCATCAAGACACTGGCGCAGGCTATCGCACCCGTTATCGGCTACAAACAAATCGCGGTATGC

.....Rv377T7.seq:.....  
CATCACCTGNTTCATGAACGGAAGCACCAGCGCTTCCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCGGCGGT  
CGGGTGCAAGTGTCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCTGAAACCAGCTTCCATATCCCGCGACGAACGA  
CGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCGTTCACACCGACCGGGCCCGGGTGTGGG  
GTGT

## Clone Rv378

.....Rv378SP6.seq:.....  
AGCTTAGCTTCCCGCCCCGGCAATAGGGCTCCAGCTCATCCGGTGTGACCAGATAGGGGCCCAGGGTGATACCGCTGT  
CTTGCCCTTGGCCTGTCCGATGCGCAGCTGGCCCTCCAGCATCTGCAGGTCCCGTGCGGACCAGTCGTTGAAAATGG  
TATAGCCGATGATCGACCG

.....Rv378T7.seq:.....  
CCNGAACAGAAGCGNGGTTCTACCGCGGTGTGCGGCCGGCGCGATATCGGCCTTTTACTAACCGAACCCGATGTG  
GGCTCCGATCCGGCGCGCATGGCATCGACGGCGACGCCGATCGATGACCGCCAGGCTTACCACCTT

## Clone Rv379

.....Rv379SP6.seq:.....  
CTCAAGCTTGGCGGACTCGACAAGCATTCTTGACAGTTGTTTTGGCTCGGCATGGTTAGCCAAGGTTCTGCGGTCCCA  
CCAGATCATCTTGGTCCGGTAGCGCTCGTCCGGGTATGCTGCCGCCGGGATTCTCGCTGCTATTACTCCCCCGAAGA  
ACGCCACCGGTCCAGCGC

.....Rv379T7.seq:.....  
GCNAGGCGGTATAGCTTCCCGTCTACCGGCGACCGCCAGCCGAGAAGCTCGTTTTCCAGTGTTGCTGGGGATTCTC  
ACGCTGCTGCTGAGTGCGTGCCAGACCGCTTCCGCTTCGGGTACAACGAGCCGCGGGGCTACGATCGTGCGACGCTG  
AAGTTGGTGTCTCCATGGACTTGGGGATGT

## Clone Rv37

.....Rv37SP6.seq:.....  
GTGTGGAACCGTGAGCGGATAACAAATTCACACAGGAACAGCTNTGACCTTGATTACGCCAAGCTATTTAGGTGAGG  
CTATATTAATACTCAAGATTGCGGTGAGCACATCGGCCCAAGAACCGCCGAAGGCACGGCGGAACGCCTGCGGCACA  
TGGGGCGACGACCAGCGGTCGGACTTCTGGGCTGTCCAGCCGGATCGCGCCGTGCGGA

.....Rv37T7.seq:.....  
CACTGTCAGTACATATGCGCCGCTCCTCCTCATCGCTGCGCTCGGCATCGTCGCCGGCGGTTCATGGCGTCACCTACC  
CAAGCCGAACCGGAACGAGAAGCTGTTCCATTATTAGGGTGTGAGCACCAATACCAGATTGCTCACCAGGAACCTAC  
CGAGCACCGGGACGGATGTGAGCCACCACGCCCATCTGGGGTGGTAGCGGGGAAATACGGCTAACGCGGCTCCGGTGC  
CGGCAGCCCAGCGCAGACCCTCGGCGGCGGACACGGCAAACAACGACGACCCATAGTTGTTCTTTGCCGGATGGCCGT  
GTTTGCGGACATATCGGGCGGCGGCGGGCGCCGCCGAGGTAGTGGCTGAGGCCCATCTCGTGCCCGCCGAATGGCC  
CCAGCCAAACCGTGTA

## Clone Rv381

:::Rv381SP6.seq:::

CTCAAGCTTTTACGGTGATCGCGCATCACCTGGTTCATGAACTGGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCAACA  
TGAGCCANCTCTCGTCGGCGGTGCGGTGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCTGAAACCAG  
CTTCCATATCCCGCGACNAACGAC

:::Rv381T7.seq:::

CTCAGAAGCCGCTAGCTGGTAGAGTCGCTGACCGGTGCACGTGGCGNCAATGTGCGCTGCCGGTTCGCG

## Clone Rv382

:::Rv382SP6.seq:::

CTCAAGCTTGCGCTCATCAAGCGCGAACAGCAGGGCGGTGCGCTGGTCGCCATGACGGGTGACGGGACCAATGACGCA  
CCC GCGCTCGCGCAAGCCGATGTGCGGGTGGCNATNAATACCGGCACCCAGGCGGCCCGGGAAGCCGGCAACATGGTC  
NATCTCCACTCC

:::Rv382T7.seq:::

ACTTCTATTTGCGACTGGTGTGCTGTGGCGGATCCGACTGCCGGCGTGGTCAAGGCCGGCCAGTTGTGGGATNCCACA  
GGCAC

## Clone Rv383

:::Rv383SP6.seq:::

GCTTGTGCTATTCCGTGGCACTGTGAGACATATGCGCCGCTCCTCCTCATCGCTGCGCTCGGCATCGTCGCCGGCGGT  
CATGGCGTCACCCTACCCAAGCCGAACGCGAAACGAGAACGTGTCCATTATTAGGGTGTGAGCACCAATACCAGATT  
GCTCACCAGGAACAC

:::Rv383T7.seq:::

CGATATTCGTGCGCCGCGTTGTCTCGACTGGGTGCGGT

## Clone Rv384

:::Rv384SP6.seq:::

GACCTCGGCCACCAAGCCGGACGCGACCGTTCGAGGTGGCGATCCGGCTTGGCGTCGACCCGCGTAAGGCAGACCACAT  
GGTCCGCGGCACGGCCANCTGCCACACGGCACTGGTAAGACTGCCCGCGTCGCGGCN

:::Rv384T7.seq:::

CCGGAAGTCTAGGGGACGACCTACTCAGCGCAAAATGTGCTAATGTGAGTCCGCCCCACCAGGGCAGATCAACCCAT  
GTCGATGATGACCTACCCGGATACCCGATTGGCGGT

## Clone Rv385

:::Rv385SP6.seq:::

AGCTTCAGTTCTCCACGACGCTTCCCAAATGAATTTCCCGATCCACAATCTCGGTTGAGATACAGGTGCCATAC  
CCCTTACTTCGGNAACGCTGGGCGGATTGGCCCTGCCGCTG

:::Rv385T7.seq:::

CCGCCTACGGGTGGAACATGCATCCCGAGACCGATGCTCGAGCGCGCACCCCACTCGCCGATGGCCGGAACCGGCTGG  
TTACCCGGGTGGCGGCTGACC

## Clone Rv386

:::Rv386SP6.seq:::

GCGGCTGGTTACGACTCCCTGTTGTGATGGACCACTTCTACCAACTGCCCATGTTGGGGACGCCCCGACCAGCCGATG  
CTGGAGGCTTACAGGCTTGGTGGCTGGCCACGGCGACCGAGCGGCTGCAACTGGGCGCNTTGGTNACCGGCAAT  
ACCTACCGCAGCCCCGACCTGCTGGCAAAGATCATCACCAGCTCGACGTGGTTAGCGCCGGTCGAGCGATCCTCGGC  
ATTGGAGCCGGTTGGTTTGGAGCTGGAACACCGCCAGCTCGGCTTCGAGTTTCGGCACTTTCAGTGACCGGTTTCA

:::Rv386T7.seq:::

GCCTTTCCGCACAATCTGTACCCAGGACNTCTAAAAAATCGAATACGACGGCGTCGCCGACTTTCGCGGTTACCCG  
CTCAACTTTGTGTCGACCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAACACTTTCATCCTGACGCCGGA  
CAAATTGACGCAGCGGTTCCGCTGACCANTNNTGTGCGTCCCACGATGACCCAGTACTACATCATTCGCACGGAGAAC

CTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGTTCAACCAAACCTTGAAG  
GTGATTGTTAACCTGG

Clone Rv387

::::::::::::Rv387T7.seq::::::::::::  
GCAGACCAACAAGATGCATCGGGATCATACGCCGTCAACTACCCGGCCAACGGTGATTTCTTGGCCGCCGCCAC

Clone Rv388

::::::::::::Rv388SP6.seq::::::::::::  
CTCAAGCTTGCCAAAGAGACCTCGTCCACCAAGCNGGACGCGACCGTCNAGGTGGCGATCCGGCTTGGCGTCCACCCG  
CGTAAGGCANACCANATGGTTCGCGGCACGGTCAACCTGCCACACGGCACTGGTAANACTGCCCCGCGTCGCGGTATTC  
GCGGTTGGTGAAAAGGCCGATGCTGCCGTTGCCGCGGGGCGGATGTTGTCGGGAGTGACAATCTGATCGANAGGATT  
CAGGGCGGCTGGCTGGAATTCGATGCCGCGATCGCGACACCGGATCAGATGGCCAAAGTCGGTCNCATCGCTCGGGTG  
CTGGGTC

::::::::::::Rv388T7.seq::::::::::::  
CCACGGCGTGGATCAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCCCGGCTTGATGTCGGCGTTAGCGC  
CGGATTCCACCACATCCCCCTTGCGAAAGTCCGTTGGGTGCAATGATGTAGCGCTTCTCCCATCGAGATAGTGGAGCA  
ACGCAATCCGTGCGGTACGGTTCGGGTCNTACTCGATGTGCGCGACCTTGGCGTTGACACCATCTTGTGTCATTGCGGC  
GAAAGTCGATCATCCGCTAAGCGCGCTTATGACCGCCGCCTTTGTGCCGGTGGTAATCCGGCCATGCGCGTTGCGTC

Clone Rv389

::::::::::::Rv389SP6.seq::::::::::::  
GGCGGCTGCGTCGGCGAGATGATCGCCCCGGTGCCACCCCGATCCGTGCCTCGGTCAGCGCCAACGTGCTTCCGGTCC  
GGCGACCACCATGTCGCATGCGCCGAC

::::::::::::Rv389T7.seq::::::::::::  
GCAATCGCCTTGCGGTCGCCGGGTTGTACCGGTGATCATCNCGGNGCGGATGCTCATNCGGCGCATTTGCTCNAAT  
CGTTCCTCGTATGCCACCTTGACGATGTCCTTCATATGGACCACGCCGATGGCCNCGCGCTNCTG

Clone Rv38

::::::::::::Rv38SP6.seq::::::::::::  
CCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAAG  
CTATTTAGGTGACACTATAGAATACTCAAGCTTCCACATCGGTATGCCAAAGCATTGCGCCGCTATCGATTTGCGGCT  
GGCATCGCCAAGGTGGACTTCTTGTCTCAGCGACGAGATCCCGTGGTGGATCCGCGGCTGCGGCGGGCTGCGACCCCTG  
CATCTCGGCGGCACCCGTGACCAGATGGCGCGCGCCGAGGACAGCTCGCGGCGGGACGCCACGCCGACTGGCCGATG  
GTGCTGGCCGCGTGTCCGCACGTGCGCGACCCCGCCGATCGACGAAACCGGCCGCGCTCCGTTCTGGACCTATGCC  
CACGTGCCGTGCGGGTCCACGCTCGACGCGACCGAGACCGT

::::::::::::Rv38T7.seq::::::::::::  
CGCGTCCACCGCAGCGTGAGATTGGTGCGCCATTCTGTCGTGGTGTAGCTGCTGTTGGCGGCGTCGCCGTATTGTGCG  
GGCCAGCCTTGTGCGGGGGCGCTTCTACCCACGAGTCGGCACTTCCGCAACCGCCAGCTCGACCGGATTACGGCG  
GCCGCAACGGCCGCCGGAAGGCGTCTCGCAAGCGCCTTATCCTTTCGAGGTTCCAGATCCTTCCGCTACGTGGGTC  
GCTCATCGGCGGGCCCGGCCGAATGAGTACAGGTGAGGGTAACCGCTACAAATGAAGTTGGTCAGTGCTGGCCAACTG  
TGTAATGGTTGCCCGGCTCGGGTCACCACGTACATTCTGGCAAGGCGGGCGAGATTGCGTTCCTCGCGTCTTGGCCG  
GTGGCGGTTCCCGGTTGTCCGTGGGCGTGTCTGTACGTGGTGTAAGTGTGCTGAACCTCCTCAGTTTGGGCT

Clone Rv390

::::::::::::Rv390SP6.seq::::::::::::  
CTCAAGCTTGCGCTGGATCTGGCGGCTGAGCCTGTTCTTGGGCAACATGCCGAGGGATCGCCTTTTCCACCACGCGGT  
CGGGGTGGCGTTGCATTAGCTACCGATGGTGCGCTTGTGCGAGGCCGCCGGGATACCCGAGTGCCGGTAAACCATCT  
TGTGCTGCAGTTTGTGCGCGCTGATGGCGACCTTGTGCGCGTTGATCACNATGACNAAGTACCCGCCATCGACATTGG  
GGGCAACGTGCGCTTGTGCTTGCCGCGCAGCAGTTGGCCGCCGCGACGCAAGGCGGCCAANACACCGT

.....Rv390T7.seq:.....

TTTGGGATGGGCAAAAAGGCGAAGCNC CGCTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGGCTAGGGCTTCTC  
GCGGGAAGGCCCGAACGTACGGCGTTTCAACACGTCGCGTCGCCCTCCGACCGCGAACATTTCGGGGATGGCAGCAACC  
TGGTAGCACCCCTGGCCGGGCGATGATCTGCAGCGTCGCCGCGGGTAGTCGCCGCCCCGGGCGGCTACAGTCTGAAACGC  
GATGACCATCGATGTGTGGATGCAGCATCCGACGCAACGGTTCCTACACGGCGATATGTTTCGCTCGCTGCGCCGGTG  
GACCGGTGGGTCTATCCCGGA

Clone Rv391

.....Rv391SP6.seq:.....

CTCAAGCTTCGTCATAAGACCATGGTGCCTTTCTTTACCCGTCCANAGTCGGGGGCATCCGCACCGGCTCGCATCG  
CATCATCCTCCACGACGGGCGCTCATCAGCTTGGGCCATTTCATGTACTTGATACCCCGCGCTGCGGGTAGGCCA  
CTGCNACAATTCAAACACGGTGTACACGGTGAATANTGTGNANATGGGCTCTGATCAACCGTCNCAAACCGGTTTC

.....Rv391T7.seq:.....

GAATTCTGCGTGACCGCTATGGGTTGCAGCAGCGGCTGGCGCCGCACACCCCACTGGCCCGGGTGTTCGCCCCGA  
ACCCGGATCATGGTGAGCGAAAAGGAGATTGCCTGTTTCGATGCTGGGATTTCGCCACCGCGAGGCCATCGACCGATTA  
CTCGCCACCGGGGTGCGAGAGGTGCCGAGTCCCGCTCCGTCGACGCTCCGACGATCCATCCGGCTTCGCGCGTCGG  
GTGGCGGTAGCCGTCGATGAAATCGCTGCCGGCCGCTACCACAAGGTGATTCTGTCCCGTTGTGTGCAAGTGCCTTTC  
GCGATCGACTTTCGTTGACCTACCGGCTGGGGCGTCTGCACAACACCCCGGTGAGGTGCTTTTGTGTCAGTTGGGC  
GGAATCCGTGCTCTGGGTTACAGCCCCGAACCTCGTCNCGCGGTGCGCGC

Clone Rv392

.....Rv392SP6.seq:.....

GCAGTTGGGAATCGCTCTGCAGCAAACCANTATTCTGCGCGACGTTTCGAGAGGACTNNTTGAATGGACGGATCTACCT  
GCCGCGCGACGAGCTGGACCGATTAGGCGTACNCCTCCGCTGGACGACTCCGGGGCACTCGATGACCCCGACGGACG  
GCTCGCGGCACTGCTGCGGTTTCANTGCCNACCGCGCCGANACTGGTATTCGCTGGGACTGCGGCTGATTCCACACCT  
CGACCGCCGCGAGCGCTGCCTGCTGTGCGGCCATGTCTGGCATCTACCGCCGTCNGCTCGCCTTGATCAGACCATCGCC  
GGCGGTGCTCTACCATCGGCGAATCTCTCTGTTCCGGACTGAANAANGCCCAAGTGGCGGCGGCAGCACTGGNCTCTT  
CGGTAACCTGCNGACCGCCCATTTGGACCGCTACCG

.....Rv392T7.seq:.....

TTGATCTGGACGCTCTGAGACGGTGATCGGNCCGAACCTGAATTGTCCGGTAATGCCAGCGCAGAAAGCANGGTGGTG  
GCCGGGCGGTGAANCCGGCGTCGGCGGCACCGTCGAAGTCGATGTGGATTGCCGGAATGGGGATGTCCGGCACGGCG  
AAGCCGTAGTTTCGCTTGTCCCGTGAGGCCCANGTGGATGGGGGAAGGATCGTGGTGTCCGGGATGATAATGGGGCCG  
ATGCCGCGGTTGAAGTCCAGTGGATCGGGAATTTCGGGAATCGTGATGCCGACGTTTCAGGCCGAACAGGCCCTCCAAG  
TTGCCTCGCCACNAGATGCCGTTGCTGAAGTTGCCCGACATGAGGGCGCCGGTGTCCACATTGCCCGAATTGGCGACG  
CCGTGTTGGC

Clone Rv393

.....Rv393SP6.seq:.....

CACGTAGGCGCGTCCATAAATNACTCCGCCGCGCTTCGCACATCCTCGTANCGATCCTTGCGGAGCAGGTCAACCGG  
GCGCTGCCCGTCNAGGAGCCGGTTTTTGGCGTGACGCACTGGCCGACACCTCGGGGGGTAAAGCGAATCCGAGAGCAG  
GAGGACNAGGTCACGAANCTGCGCCAGCCGGTTCGTACCGCTCAGGGCGGATGTCCCGGTCGCCACCCCGGTACCGC  
CCGATCGGACACCTGTATGACCGCGGCGACNTCGACCTGGGTGACGCCGAAGGGTTTCAGGGCATCNACNATCTCGCT  
GGCCTCGACCGCCCGGTCCAGGGTGACCGCCATCGTGTTCTCTCCGCAACTTCGGTTCTACTACCGTAAACGCTACC  
G

.....Rv393T7.seq:.....

CGGGGAACGTTCTCGCACACCTGGTTCGTGTTGCGGGAATTACTCGGACANCAAAACGTCAAGAACTACGACGGCAG  
TNGGACAGAAACAGGCTCCCTGGTGGGCGCCCCGATCGAGTTGGGAAGCTGATATGTGCTCTGGACCCAAGCAAGGAC  
TGACATTGCCGGCCAGCGTCGACCTGGAAAAAGAAACGGTGATCACCGGCCGCGTAGTGGACGGTGACGGCCAGGCCG  
TGGGCGGCGCTTTCGTGCGGCTGCTGGGACNCCTCCGACAGTTTACCAGCCGGGAGGTCGTGCGCTCGGCCACCGGG  
CGAATTTCCGGTCTTCGCCGCGCCCCGGGATCCTGGGACCGCNGGCGCGCTGTT

Clone Rv396

.....Rv396SP6.seq:.....

CTCAAGCTTTGTCCGACAAGCGTTCGCGGGCGGTGACGAAGCGAACGTCGGTTGGCCCACTGCGGGTCGATATTGCCG  
CCAGGGA

.....Rv396T7.seq:.....

CGTCAGCACGGCGACGTCGCGNTACGCCGAGCAGTTACACAATCGCTCTGCAGCAAACCAATATTCTGCGCGACGTTT  
GAGAGGACTTCTTGATTGGACTG

## Clone Rv39

:::Rv39SP6.seq:::

CTGCATCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTAC  
GCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCGCGCAGCGGGGGTTGACCCGGTTACGCGCGTCATAGC  
TGGCCAATCTGGCATCGTCGATCANCATGTGGTGGGGGGTGACCTCGGCGGTGATCGAAATACCCTGGTCTTATCCC  
ATTTCAGGATTTTCGACGGTGCCCGCGGCCGACGCGTGACAGATGTGCACCCGGGCGCCGGCGTCACGGGCCAGCAAGG  
CGTCGCGGGCGACGATCGATTCTCGGCGGCCCCGCGGCCATCCCGCCAGGCCAGCCGCGCCGCCATGGGTCCCTCGT  
GCGCGACGGCGCCGACCGTCAGCCGGGGCTCCTCGGCGTGCTGGGCGATCAGCACGCCCAAACCGGTG

:::Rv39T7.seq:::

CCGACGCGCACTACGTGCTGGTGTCCACCCGCGACCCGACCCGGCAGAGCTACGAGCTACCGCATCGTCGATGGCG  
CTGTACCCGAGGAACCTGTCAATGTCTGTCGAGCAGTACTGAACCGTTCCGAGAAAGGCCAGCATGAACGTACCCGTAT  
CCATTCCGACCATCCTGCGGCCCCACACCGGCGGCCAGAAGAGTGTCTCGGCCAGCGGCGATACCTTGGGTGCCGTCA  
TCAGCGACCTGGAGGCCAGCTATTCGGGCATTTCCGAGCGCCTGATGGACCCGTCTTCCCCAGGTAAGTTGCACCGCT  
TCGTGAACATCTACGTCAACGACGAAGACGTGCGGTTCTCCGGCGGCTTGGCCACCGCGATCGCTGACGGTGACTCGG  
TCACCATCCTCCCCGCGGTGGCCGGTGGGTGAGCGGACACATGACACGATACGACTCACTGTTGCATGCCCTG

## Clone Rv3

:::Rv3SP6.seq:::

TGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG  
CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGCCGGGAGGGTGCATGGCCGACTCGGATTTACCCACCAAG  
GGGCGCCAACGCGGTGTCCGCGCCGTCGAGCTGAACGTTGCTGCCCCCTGGAGAACCTGGCGCTGCTGCGCACCTG  
GTCGGCGCCATCGGCACCTTCGAGGACCTGGATTTCGACGCCGTGGCCGACCTGAGGTTGGCGGTGGACGANGTGTGC  
ACCCGGTTGATTGCTCGGCTTGGCCGATGCCACCTGCGCCTGGTGGTGCATCCGCGAAAAGACGAAGTTGTGGTG  
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:::Rv3T7.seq:::

GGAAACACCGNCGCCGTCGTGGCCACCAACCCGCGACCCAGCACCGTGACCCGGACCGGGGTGCCGCGGAACCGGTC  
TTGGCCAATTGCCGCGGCACCAAGCCGTGCGCGCCATGGCGAACAGCACGCGGCATTGCCCGAGCATCAACACCATC  
ACCACCGTGGTAAGCCCGGCCAGCGCGCCGACGGAGATGATGCCGCTGGCCAGTACACCCGTTGGCCTGGAACGCG  
GTGGCCAGATTTGCCGCGCCGCGGCCCGGTACGGTCCGCGAGTTGGGTGTATGGAACCATGCCGACAGCACCCGAT  
ACCGCGACGTAGAGAAGGGTCACGACCCCGAGCGACGAGAAATCCCTCGAGGGACGTCTCGTTGAGGACGCTTGGTC  
TCCTCGGCCATGGTGGCCACGATGTCAAACCCGATAACCGGAAGAACACGATCGATGCCCGGCCAGCACGCCGTA

## Clone Rv40

:::Rv40SP6.seq:::

CCTGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTA  
CGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGCTTCGGGCGTGGCCTCGGCCAAGAAATCGTCGACGC  
CGGCCTCCTGTGCAATCGCCTTGGCGGTGCGCGGTTGTCACCGGTGATCATCACGGTGCGGATGCTCATTGCGCGCA  
TTTCGTGGAAGCGTTCCCGTATGCCACCTTGACGATGTCTTCAGATGGACGACGCCGATGGCCCGCGCGCTGCTGT  
TATCGGTCCATTCCGCAACGACTAGGGGTGTCCCCCGCGGAGCTGATGCCGTGACAATGGCACCCACCTCCTCAG  
TGGGGTGGCCACCGTGATCGCAAACCACTTCATCACCGCAGCCGCGGCACCTTGGCGATCCGAACGGATGCGCTC

:::Rv40T7.seq:::

TTCTGTCGATGGCGCCGCCCCGGCTACGGTTTGACCTGTGGGTGTGCAATTGGGGTCAAATTCCGAGGTGCGCGCGCT  
AAGAGTGGTCATCCTGCACCGCCCGGGGGCCGAACCTGCGCCGGCTCACACCGCGCAACACCGACAGCTGCTGTTGCA  
CGGCCTGCCCTGGGTATCCCGCGCGCATGACGAGCACGACGAATTCGCCGAGCTGCTGGCTTCCCGCGGTGCGGAAGT  
GCTGTTGCTGTCGACCTGTTGACTGAGGCACTACATCACAGCGGGGCCCGCCGATGCAGGGGATCGCCGCTGCCGT  
CGACGACCGCGGCTGGGACTGCGCTGGCGCAAGAATTTCCGCCCTACCTGCGTATCTCGACCCAAGCANGTGGCG  
CATGTGCTGACGCCGGCATGACTTCAACGAACCTCCNTCCGACACGCCGAACGAAGTGTCTGTTGGTGTGCGTATGC

## Clone Rv412

:::Rv412SP6.seq:::

GCGGCGAGTGTGGTGGGTGCCGAACAGCAATCCAACGACGCACTGGCGGAGAGATACCACTTGCTGTACTGGAAGCAC  
GTGCTGATGATCTCCCGTGAATGTGCCTCGCCGCGCTCTATCGAAAACAGTGAGCATGCTGCG

.....Rv412T7.seq:.....

CAACCGCGCTCGGCGCGTCTGGGCCTTCCGCCGGCTCCGCCGACAATTCTATCTCTGGATCAGCGGGGCTCTCCGGGC  
CGGCCTCCGCGAACTCAACAGGCCGCGCCTTCCGGCCGAAACATTCCTAGCCATATATGATCGCACCTCGATACACG  
ATCTGGCGGCAACACCGCAAAGCGTCCGACGGGCCCAACCTCCGCAATTCAGGTATCCGGG

Clone Rv413

.....Rv413SP6.seq:.....

GAAGGTCGGCGAAGGTGTGGCTGGNTGCCGATCACGAATCCAATGATGCAGTGGTCGGAAGATATTAGCCACTTGCTG  
TTCTGGAGACAGGTGCTGATGATCTCCCGTGAATGTCCCTCGACTCCGTCTATCGAAATCTGTGAACA

.....Rv413T7.seq:.....

TCCTGCGCTCTGGGCCATTCTCGGGTCTGCCGACAATTCTATCTCTGGATCTGTGGGGCTCTCTTGGCCGGCCTCNGC  
GATCTCTTCANGGCGCGCCTTCCGGCCGAAACATTCCCTATCCATATATGATCGCACCTCTATACACCGTTTGGCGGC  
AACACCGCAAAGTGTCTGTCTG

Clone Rv414

.....Rv414SP6.seq:.....

AGCTTTACGCTGGCGTATCAGCGTTGGGGCCGCTGCCATTTCGGTCGCCCCAACGCGTTGCCAGCTCCCTGCGCTGTCA  
GGGCTTGCGCGCCAACTGGCCACCGCAACAACTTGGCTGAGCTTGATC

.....Rv414T7.seq:.....

CTCTATCTGGCGTCACATTTCGCAATCTTAGATTGCAGATATCGATAAAATCACCCGCGCGACAAGACCGCCATGTCA  
TCCTTTCGATGTTATTTCCGCCGGCTGGGGAAAGCGCAACGACGTTGCCTACACGTTCCGCCGT

Clone Rv415

.....Rv415SP6.seq:.....

AGCTTTNCCTTGCATCTGCACCCCGATCCACGTGAGCCACGTCCGGCGTTCTCCACCAAGAAGTTGCGGGCATTCCTCT  
TGCCCTGGCCGAGCTGCTCGCCCTCGTAGGTGAACCAGGCACCCGACTTGCGGATGAGGCCCTGATCCACACCCATGT  
CGATCAGCGAGCCCTCCCTGCTGATTCCTTGGCGTAGAGGATGTGCAACTCGGCCTGCTTGAAGGGGGGCGAACAGT  
TGTGCACGACAACCCCTTCGGCGACGAGGGTGTGCACTTCCTCGACCTCGAGGTCGAACGTTCTGTCGCCCGCGCGTTG  
GCAGCACTTCTCGGATCACGGAATAGCGGANTTCTTCCGCCAGCATGTGCTGCAGGAATTTGTCTCCAGGGCATCCG  
CGAGCGCCTGCACGCG

.....Rv415T7.seq:.....

ACTGTCNAGGGAATGCTTCGCGAGCATCTACCTGCAGTCGCTTGTGCATAAGCGGACGGCCCNACCTGTTCTGTTCGG  
GGACACCAGACGCGGGAGCACCGGCAGTACGGCGAAAGGTTTGAAGCGGAAGGAGTTGCGCAAATCGGGGCGCCCCAAC  
ACCCGTCCGCAAGACGCGGTCAACGACCTGTTTCAGGCGATCAGGGTCACCGACTCACCTGCACTGAGAACAAGCGAT  
CTGCTGATCTGCCAGAAGATGGACATGAATGTCCACGGCAAGCCTGATGGCCTGCCGCTCTTCCGGGAATGTTTGGC

Clone Rv416

.....Rv416SP6.seq:.....

TGAATTATGATCCCAGACAACTGCATCANTTTAGCCGCGTCGNGATGCTATCCGCCGACGGTTTGGANCNGGTCCGT  
GTCGTTTCGTGTTGATCTCACCCGAAGTTGTGTCCGCCGCGCGGGGATCTAGCGAACGTGGGATCGACAATCAGCGC  
CGCCAAACAAGGCGGAGCGGCTGCGACCACGCAGGTGCTGGCCGCGGGCGCCGATNAGGTGTCAGCGCGCATCGCGGC  
GCTGTTTGGTATGTACGGCCTGNAATATCCGGCGATCAGTGCGCAAGTTGCCGCGTATCACCANCAGTCCGTGCAG

.....Rv416T7.seq:.....

AACGGGGACCNCAAGAAACATTCAANAACGAGGGGTGCTACCAACGTGCAACCGACGGTTGCCAGCCGGGGCCACG  
ATATTGCGTGCTCGAGGGTCCGCTGTACCCTCACCGAACGTGAGTCCACACCGCGGAGGCGGGCGACTCTGGCGTGC  
TTAGCAGCCGAGCTCAAGGTGTCCCGCACCACTGTCTCGAATGCTTTTAACCGACCGGATCAGCTCTCCGCCGATCTA  
CGTGAACGAGTGCTTGCCACGGCCAAGCGACTGGGCTATGCCGGACCGGATCCGGTGGCGCGATCGTTGCGGACCCGC  
AAAGCCGGTGCGGT

## Clone Rv417

:::Rv417SP6.seq:::

AGCTTTGGAGCCNCNCCGANCCNCCGGTACGCCCCGCCACCGCCGTACCCGGCACCCGACCCCTTTGAGCCGTTGCGC  
GTGGCCGCGGTGGANCTGGCCGACGAGGGACTGATCGTGCTGGGCAAAGTGGTCGATGGCACGCTGGCCGCGCATCTG  
AAGGTCGGCATGGAGATGGAGCTGACGACCATGCCGCTGTTGCGCCGACNACGACGGTGTGCAGCGCATCGTCTACGCG  
TGGCGGATCCCATCGCGCGCCGGCGACNATGCANAGCGCANCGATGCTGAGGAGCGGCGCCGATGAGGATGAGCGCGC  
CGGAACCCGTTTACNTCCTGGGTGCCGGTATGCACCCGTGGGGGAAATGGGGTAATGACTTC

:::Rv417T7.seq:::

TTCTCNCATCGTTCTACTNNGATGGGACGCTGCTGCCCGAGGCGATCCTGGCCAACCGGCTCTCGCCGGCGCTGACC  
TTCGGCGGGGCGAACCTGAACTTCTTTCCGATGGGCGCTTGGGCCAAACGTACCGGGGCTATCTTCATTGCGCGTCAG  
ACGAAAGATATTCCCGTCTACCGCTTCGTATTACGTGCTTACGCCGCGCAGCTGGTGCAAAACCATGTCAACCTCACC  
TGGTCGATCGAAGGGGGTGGACCAAGAGGCTACGGCCACCGGTGTTGCGGATCCTGCGTTACATCACCGAT  
GCGGTCGACGAAATCGACGGTCCCAGAGTGTATTTGGTGCCGACCTCGATCGTGTACGAACAGCTGCACGAAGTGAA  
GCCATGACCACCGAAGCCTATGGCGCCGTGAA

## Clone Rv418

:::Rv418SP6.seq:::

TTCTTCCGGGTACCGCTGATCGGCGGCACCATCACGCACCCGGTGCAGGGCGAGGCGGCCCGGTTGTTGTTGCTA  
CGGCCGGCCAGCCCGGGTACCGGTGTGATCGCCGGTGGTGCGGCCCGCGCGGTGCTGGAATGTGCGGGGGTGCACGAC  
ATCTTGGCCAAGTCGCTGGGCAGTGACAACGCGATCAATGTGGTGCACGCCACCGTGGCCGCGCTCAAGCTGCTGCAC  
CGTCCGAGGAGGTGGCGGCGCGCCGCGGTTTGCCAATAGAAGACGTCCCCCGGCCGGGATGCTG

:::Rv418T7.seq:::

GTCGAAAGTGACCATCTCTACCTTGAGTGCCATACCGCCCGACCTATGCCTCGGATAGCTCGGCGGAAAGAAACGCT  
TGCACTGCCGCCGAATAGGCGGCTACGTGCTGAGCGCCCATCAACTCTCGCGCGGAGTGCATCGCCAGCTGGGCGGCG  
CCGACGTCGACCGTGGGGATTCCGGTGCGCGCCCGGCCAACGGCCCGATCGTGCACCCGACGCGCAGATCGGCGCGA  
TGTTTCGTAACGCTGCATAGGCACTCCGCGCGCTGGCAGGCCAGTTGCGAAACGCCCCCGCGGGTGCCTTCCGTGCG  
TTGGCTTTACCGCAAATTTGGGGTTGCCCCCT

## Clone Rv419

:::Rv419SP6.seq:::

AAAGCCACGAAACGATTGCCCTACTGCCGAATCGGGGAACGGTCCTCGCACACCTGGTTCGTGTTGCGGGAATTACTC  
GGACACCAAACGTCAAGAACTACGACGGCAGTTGGACAGAATACGGCTCCCTGGTGGGCGCCCCGATCGAGTTGGGA  
AACTGATATGTGCTCTGGACCAAGCAAGGACTGACATTGCCGGCCAGCGTCTACCTGGAAAAA

:::Rv419T7.seq:::

TTTCGCCACCGCNAGGTCGTGCGGTTCCAGAAAAGCGTGGTTTCGCGGGGCGCGAGGATTCGACGGTCCAACCTGACC  
AGCCGGTCCCGCCACCGTTAGGCAGGATCGCGGTGTCTATATGTTGCGCCTCGGCATAAACGCCATTGCTGCGGTGA  
AAATCGGACATCTCGCCGATTGCCACGTCTACATGATCCGCTTTGTCCGCGCGGGTTCGTTGACAAACCGGATGTCN  
GCCTCCTGGGAAGCGGTGGC

## Clone Rv41

:::Rv41SP6.seq:::

TCGCCAAGTGGATTCTGTGCTCACCNACGAGATCCGTGGTTCGGATCCGCGNGCTGCGGCGGGCTGCGACCCCTGCATCTCG  
GCGGCACCCGTGACCAAATGGCGCGCGCCGAAGCAGACGTCTCGGCGGGACGCCACGCCGACTGGCCGATGGTGCTGG  
CCGCGTGTCCGCNCGTCNCCGACCCCGCCGCATCNACCAAACCGGCCGCGTCCGTTCTGGACCTATCCCACGTGCC  
NTCGGGGTCCACGCTCGACGCGACCGANAAACGTAACCAAGCGTCTCGANCGGTTGCCCCCGGCTTCCGTGACATCGT  
GGTGGCGGCGCGCGCGT

:::Rv41T7.seq:::

GTACCGTCACCATGATCGCCCCCATCGGCATCGGTGAGCTGATAGATCCCAGCCGGTTTCGCCAACCCCGGAGCGATC  
TTGGCGCGCTGCTNGTNGTCNCTGANACNTAGCCACCAACAGAGCCCGGTGTGCGACAAGANGACTGATCGGATCTCT  
CCGGACACNTCGAGGGGGTTCNCCAGGAGNCCGGGCGCCACCCCGAGGTAAGCCTCCGCCCAGCCTCACACCGCGACCG  
GGTATCNCAAGTCGCGCAATAANCCACACCTCCTCGGACCCACGTTGTATGCGGCTGGT

## Clone Rv42

:::Rv42SP6.seq:::

ATACTCAAGCTTAGACCTCACTGATGTGGCGGGACGCGGGAGATAACCGCGGTTGAGCCGTTCAACAGTGGTGGTTC  
CCACACCAGTTGTTTGCCTTTGCGAAGTAAAGCGATTTCGATTTGCTCGAAAAGAGGGCTGGCTGCTCGTGAGGGACAT  
CCATGGCCGATACCTCAGCGATCTCAACGGTCAAGCGACTGCATGTTTGGCGCAAGGTATCGCTAAGCATAGGTTTCGT  
GACGGATTTGACAGCAAGAGCTTTCAAAGATTGCTGTCCACATANTGATTTCGCATCTCTACACCTCTTCGCCGGTGC  
TGTCAAGAGCCATTCTGAATCAGTTATCTCGCTCGTGCTTGAANAATTTTCCCAGCCTGCGTTGGACAAACCGCGTC  
GCCAAAGCGGT

:::Rv42T7.seq:::

AGCTTCCCGAGAAACAGTGCATTCCCTAAGCAGCCCGTTGTACGCCGATGAGTGAAGAGTGCACGCAATCGCCGGAA  
TCCGGCAAAGCCCTGCACAAGCGAAATCAACCCGGAGGCTGACAAGGCAACGTCGGTGATCCGTACCGCCTGGTTGGA  
CAAACGGCAGAAGGCGGCCCTCGTCCGGTCCATCTACGCCGAGCACACTGGTGATAGCGCGCATCGGCATCGGTGCGGC  
CACGGTGGAGACGACGTCCGCGGGCGTCTGGGTCACTAACC CGCCGACCAAGTTCTCGGGCAAGCTGGTCGACCATCGG  
GCGCCACGTCTCCAACGCGCCACGCGCCATACCTGGTGCCAGTTGCTTGCGCATCCGGGTGTGCGCCGGCGGATCGGA  
CGTCGCAGAAACGCAGCCACCCCGTGAGAAGTGACCCACGGCGCTGGACACGTGTCTGGTTAC

## Clone Rv43

:::Rv43SP6.seq:::

CGGCCGGGATGTGCGCAATGGCAGGTTGTCGCCCGGCTTGATGTGGCGGTTAGCGCCGGATTCCACCACATCCCCTTG  
CGAAAGTCCGTTGGGTGCAATGATGTANCGCTTCTCCCCATCGAGATAGTGGAGCAACGCAATCCGTGCGGTACGGTT  
CGGGTTCGTACTCGATGTGCGCGACCTTGGCGTTGACACCATCTTTGTCTATGGCGGCGAAAGTCGATCATCCGGTAAGC  
GCGCTTATGACCGCCGCTTTGTGCCNGGTGGTAATCCGGCCATGCGCGTTGCGTCCACCGCGACCGTGCAGCGGGCG  
CACCAGCGACNTCTCCGGGGTTGACCGGGTGATCTCGGCGAAATCAGATACGCTGGCGCCGCGACGACCGGCGTCTGT  
GGGCTTGTACTTGCGAATTGCCATGGTCTAATCAGGTCTTTCTCTCACCTCTCGTGC CGGGGCTAGGGCGCATTTGCTT  
GCTCCT

:::Rv43T7.seq:::

TAGCGGTGTAACCAACTCCCGGGTCAACCCGCAAACCTCTTGCGGCAACAGCACCGTTCGACGCGTCAACCGGGCTG  
CCCGGAATCCTGTGGATGGGCATCGAGTGCATGGTCACGACGTCCCCGACGCGCGCGGTGGCAACGACAAGTGGCCCG  
GATGCACCACAAATGACGGCCGCACACCGTGGGGACGGCCAGCAGAGACCGTGTGCGCGAAGTCGACGCTAATGC  
CGTAGGCATTGGCCGTCAACACAGGCGACGCCCGCGTACCACCGAGTCCACGNGGTTGGGCGGTCTCCTCGGCCAA  
CCAGGCGTGAACCCGGCGGATCCGAATGCAGCAAGACCGTGGGC

## Clone Rv44

:::Rv44-2ndSP6.seq:::

CCATTGGTTCGGTGTGCGCATACCANTACNACGCGCCGGGCACCTGACGCGGCGGCCGCAACCATTCGGTGGCCATCGC  
CATCGTTCGCCACCCGGTCAACGGACGCACCTTCTCCTGGCCGACCTAGTGCGCCACCCGCCCGCTTGGTCCCAT  
CGATCCGCTCAACATGAGCAGCGCAACCGGTACATGACATCTGCTGTGGAACCAAGTACANATTCCGCCCGC  
CCATGATGATCNTCGACCGTCTCCGGATTTCGGT

:::Rv44-2ndT7.seq:::

GCCGGCCTGGTCAAAGGGGCGTCCGAAGGANCCGGGCTGGGTAACAAGTTCTGGCTCATATCCGCGAATGCGACGCC  
ATTTGTACAGGTGGTGC GGTTGTCGTCGACGACNACGTGACTCATGTACCGGACGGGTTCGATCCCCAGTCCGACATT  
GAGGTCGTCGAGACCGAGCTGATCCTGGCAGATCTGCAACCTGGAGCGGGCCACGGGCCGGCTGGAGAANGAAGCN  
CGCACCAACAAGGCGCGCAAGCCGGTCTACGACCCGGC

## Clone Rv45

:::Rv45SP6.seq:::

GATCCACTGACCACGATGACATATCGAAATGCTCGACGATTCGATGGCGATCAAGGCCACGATGCCCTGGCCGTTGG  
GCGTATCTGGTGGATGGTGTACCCGCGGTAGGTTCCCGTGATCGTGTGCGACCCAGTCCACGCGATGGGCGGCGAGGT  
CGTCGGCACGCATCACCCCGCGTNTGCCGCGAGTGCGCCTCGAGTTTGGCGGCCAGCTCTCCCCGGTAGAATCTC  
ACCGTTGGTTCGCCGCGATCTTCTCTANCGTCGCCGCGTGGTCAGGAAAGGTAAACAGCTCACCGGGTTTCGGCGCTCG  
TCCGCCGGGCATGAACGCATCTGCGAATCCGGGCTGGGATGCGAACAACGGACCTGTGCCG

:::Rv45T7.seq:::

TCTACTGCCGAATCGGGGAACGGTCTCGCCACCNGGTTCTGTTGCCGAATTACTCAGGACACCGAAACGTCGAG  
AECTACGAGCGGAGTTGGACANAATACCGCTCCNNGTGGGCGCCCCCATCGANTTGGGAAGCNGAAATGTGCTCTGG  
ACCCACCCCAAGATGACATTGCCGGCCGCCCTCCAATGGAAATAGAAACNGTGATCACCCGCCGCTTCTTGAAG

GAATGGCATGCCCTGGGCCGGGCGTTCTTCCGCTGCCGGACTCCTCCCACCAATTACCCGCCGAAGGCGTCCCGTCT  
GC

## Clone Rv46

.....Rv46SP6.seq:.....

ATACTCAAGCTTCTGTCAACCGAAATCCCGCATGGGATAACGGGTTTAGATTTCGACAACGGGACCGTGTCTCAACA  
AGCCGGTCATCAGCTGGGCCGGCGACAACGGTATCTACTTCACCCGCTTTCGCCCGT

.....Rv46T7.seq:.....

CTGGCTCAAGCGCTCGGCGCGCAGGTGAACTCGGACCGGCTCGACGTCGCCGAACGCGAGGCGGTGCTGGCCCACGCC  
GACGCCGTCGTCGACATATCGGCACCGTGCACAAGTCTACAACAACGCCGGCATCGCTACAACGGCAACGTCGACA  
AGTCGGAGTTCAAGGACATCGAGCGCATCATCGACGTCGACTTCTGGGGCGTCTCCACGGGCCC

## Clone Rv47

.....Rv47SP6.seq:.....

CCGCCCTCCGCATTATGGGTCAAGAACCATCGGGTCGGACTTCTGGGCTTCCAACGCTCGCGCCGTCCCN

.....Rv47T7.seq:.....

CCGTGGCACTGTGACACATATGCGCCGCTCCTCCTCATCGCTGCGCTCGGCATCGTCGCCGGCGGTTCATGGCGTCACC  
CTACCCAAGCCGAACGCGAAACGAGAACGTGTTCCATTATTAGGGTGTGAGCACCATAACAGATTGCTCACCAGGAA  
CTCAGCGAGCACCGGACGGATGTGCGCCACACGCCCATCTGGGGTGGTAGCGGGGAAATACCGCTAACCGCGGCTCC  
GGTGCCG

## Clone Rv48

.....Rv48SP6.seq:.....

TACTCAAGCTTGTCCAAATATCGAAGCGTCGGGTGCGAGGCTCGGTGCGCAGCTCCAGCAAAACCCGCTCCACCCCT  
AGATGCCGGTATCCCTCAAGGTCTTTATCCGCCGCTTCACCCCACTGGCACACGGTCACCGGCACGTCGCCCCCGGCC  
ATGGCGCGCAACCGCTGAAGCGGACCCGACAGCCGCTGCGGTGATGGACTGATCGCGATCCACCCGGCATTGAGCCGG  
GCTATCCGCGGGAAGTTCGCCGGTCCCCCGCCACATACAGCGGAGGATAGGGCTTTGTACCCGGCTTCGGCCAGCAG  
TAGATCGGATCGAAGTCCACATATGTCCCATGGAATTCGCGCTGCTCCTGCGTTGAGATCTCGATTATCGCGCGCAAC  
CGCTCATCGATCACAGTCCGCGCACCGCAGGGTCCACACCATGGTTGGCGACTTCTTCGCGCAACCAGCCACACCCA  
CGCCGAAACGAAACCGTCCCTGCG

.....Rv48T7.seq:.....

CAGGCATGCAAGCTTGGCCAACCTCCTCATCGGACTTGAAGGTGCCGTCTCGTTGGCGGGCCCTGCTCCACGGCACGTT  
GATGGCACCAGGAATGTGTCCGGGCGCTGGCTTTGTTCTCGCGGAGGTGCGCGGGGGCCAGGATCTTGCCGGAGAA  
CTCGTCGGGAGAGCGCACGTCGATGAGGTTCTTGACGTTGATGGCCGCCAGGACCTCGTCGCGGAATGCCGAATCGT  
GTTATCCGGCGGGGANGCGGTGTAGGAAGTCACCGGCCGGCTGACCGGGTGGTGGACAGCGGGCGTCCGTCGAGCTC  
C

## Clone Rv49

.....Rv49SP6.seq:.....

ATACTCAAGCTTCAAAACAGGCCTGTTGTGGGCGCACCCGGCTCGCCGAGTTCTGCACGCACCGCCTCAAGTGCGGCC  
CGCACCGCCGGCATCTCCCGGTACGCAGGGCCGCGGCCCGCGCCGACGCGAGGCGTGTTCGCGCAGTTTCGCCGTCA  
ATGATGCTGACCTGATCGGCCACCCGGCGGTCTCGGCGTCTGCCGTTCACTAATCGCGGTGCTCAGCAGCGTCTCG  
ACAGCCACCAACCCGAGTGGAGACCAGATGCNCCACCACGGACCGCAGCGATGCCAGTCACCTACCCGTCC

.....Rv49T7.seq:.....

CAGGCATGCAAGCTTTGCAGTTGCTGAGTAATGTCGGCCAACGTCACCACAATCGCGATGAATTCAATCATGCCGCCC  
AGGGCGGCCAACCAATGGTGGCCGCGAGCGGCAGCTCGATCGCAGCGGAGGTTGCCGGCCGCCAGTTGATTACG  
AACAGGGTGAGGTATAGGCGGGCAGGATAGTGACGAAGGCAAGACCTAGATCTGCCGTGCGAAGAAGAATCGAGTAT  
CCGGTCGACACAACGGAAGCGAAAGTGTCCGCGATGTTGATGAGCGTCGCCGTTGTGGCGGCGGTGGCGGCGGTAGC  
ACCGTCCGCACATACCGCGGGGAACGCGGGCATCCGAATTTGGGGCAGGGTGTTCAGGGCGGCTGGCAACTACCATGA  
ATCT

## Clone Rv4

:::Rv4SP6.seq:::

CCGGCTCGTATGTTGTGTGGAATTGTGACCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAAG  
CTATTTAGGTGACACTATAGAATACTCAAGCTTGGCCGCAGGGCCGAGTCGATTGGTCGCGGTGCGCTCGACAGTTAG  
CTTATGCAATGCTAACTTCGGGGCAAAGTTCAGGCGGATCGGCCGATGGCGGGCGTAGGTGAAGGAGACAGCGGAGGC  
GTGGAGCGTGATGACATTGGCATGGTGGCCGCTTCCCCCGTCGCGTCTCGGGTAAATGGCAAGGTAGACGCTGACGTC  
GTCGGTCGATTTGCCACCTGCTGCCGTGCCCTGGGCATCGCGTTTACCAGCGTAAACGTCCGCCGGACCTGGCTGCC  
GCCCCGTCTGGTTTCGCCGCGCTGACCCGCGTCGCCCATGACAGTGCAGCCCTGNACCGGGCTGGCC

:::Rv4T7.seq:::

GTGTGCTGTCAATTCAGAGCTGAGCCTGATGCACTCAACTTACTGAGCATGCTAACGCTGGTCGTGCGGGTCTTGTTT  
CCGCGTGTGCGGCAGGGCACACGCTCGGGGCGTAGCTGGGAGAGGCCCCGGTCAAGCCCGGAGAGCAGTGCTCAGTCCG  
CCAGCTTGACCGACTTTCGATGAGAAGCGGCTTCTCGCCGTATTGAACTGGCGTGCTGACGGTCGCTGAGCAGCGCTC  
GCCGAGTGCGGCCGCTGATTCTTTTCATCGAGCCAGGAGGCGCATTCGTGTTTCGGCCGCTGCGGGTCGGCCCCATCGT  
CGACGCGATCCGTACCCACTCCTCGATCAGGTCTGCCTCATCGAACGGGCCAACGGTGCTGTGCGAGTAAGTGTGCG  
TGGGCACGCGAGCCGGGTGCTGTGGTACACCCACCGTTGCATGAACAA

## Clone Rv50

:::Rv50SP6.seq:::

ATACTCAAGCTTCACCAGGCGCCGGCGGGCCGCGGCCAAGCCAGGCAGCCGCGCTCGGCGCGTCGGGGCCTTCCGC  
CGGCTCGGCCGACAGTTTCGATCTCTGGATCGGCGGGGCTCTCCGGGCCGGCCTCGGCGACCTCAGCGGGCCGCGCCTT  
CCGGCCGAACCATTCCTAGCCATAGATAACCGCACCTCAATGCACGGTTTGGCGGCAACCCGG

:::Rv50T7.seq:::

AGCTTCCGTACGACCCGCCCTCGCCGGTGCCGGCGCCATCGGTCTCGGATCTCATGACGACGTACGTAGGCCCGC  
TAGCCGCGAGCGGGCGCGGTCAACTGGCGAGGCGGGCGGCGACGTGACTGAGCTGGCCGAGCTGGACCGGTTACCGCG  
GAACTACCGTTCTCGCTCGACGACTTTCAGCAGCGGGCTTGACGCGCGCTGGAACGCGGCCACGGTGTTGCTGGTGTG  
CGCGCCGACCGGCGCTGGCAAGACGGTGGTCG

## Clone Rv51

:::Rv51SP6.seq:::

ATACTCAAGCTTGCCGGGACCGCGGAACGAACCGGCGGTTCTTACCGCGGTGTGCGGCCGGCGCGATATCGGCCTCC  
CGACTAACCGAACCAGATGTGGGCTCC

:::Rv51T7.seq:::

ACGTTGGCTCTGCCGGAACGTATTTCCAGCGGCACGCATTCGGCGTGGGTGCCGGGCGCCGAGTTGCGTCGCTGGGAT  
CACGCAGCAGTCGCCGGCGGCTGCCGTGGGCTATGAATTGCACCGAGCCGAAAATCCNCAC

## Clone Rv52

:::Rv52SP6.seq:::

ATACTCAAGCTTGTGATATCCGTGGCACTGTGACATATGCGCCGCTCCTCCTCATGCTGCGCTCGGCATCGTCG  
CCGGCGGTGATGGCGTCACCTACCCAAGCCGAACGCGAAACGAGAAGTGTTCATTATTAGGGTGTGAGCACC  
ACCAGATTGCTCACCAGGAACCTACGCAGCACCAGGACGGATGTGAGCCACCACCCCATCTGGGGTGGTAGCGGGGA

:::Rv52T7.seq:::

CGTTGGTAGCCCGATATGCATAGTGTATCTTACTGAACATGATTTCCATTATGGAGCCCGGGGTGCCGGCAGCGCGAA  
CGGTGCGCCGTGACGCGGGCGGCACTGACCAGGTGTTGCGGGCGAACATCGGCCCGGCTTCGGATTCCGGTCCGG  
GTACCGGGCGACCCACCGCTTCGAGGTA

## Clone Rv53

:::Rv53SP6.seq:::

ATACTCAAGCTTGGCCAACTCCTCATCGGACTTGAAGGTGCCGTCTCGTTGGCGGCCCTGCTCCACGGCACGTTGAT  
GGCACCAGGAATGTGTCCGGGCCGCTGGCTTTGTTCTGCGGCAGGTGCGCGGGGGCCATGATCTTGCCGAAAACTC  
GTCGGGAGAGCGCACGTGATGAGGTCTTGACGTTGATGGCCGCCAGGACCTCGTCGCGGAATGCCGAATCGTGTT  
ATCCGGCGGGGAGGCGGTGATGAGGTACCCGGCCGGTGACCGGGTCGCTGGACAGCGGGCGTCCGTCCAGCTCCCA  
CTTCTTGCGGGCGCGGTCCAACNACTTGACTTCTCCTGG

:::Rv53T7.seq:::

ATATCTTAAGCGTCGGGTCCCGAGGCTCGGTCCGCGAGCTCCAGCAAAACCCGCTCCACCCCTAGATGCCGGTATCCCT  
CAAGGTCTTTAGCCGCCGCTTACCCCACTGGCACACGGTACCGGCACGTGCCCCCGGCCATGGCGCGCAACCGCT  
GAAGCGGACCCGACAGCCGCTGCGGTGATGGACTGATCGCGATCCACCCGGCATTGAGCCGGGCTATCCGCGGGAAGT  
TCGCCGGTCCCCCGCCACATACAGCGGAGGATAGGGCTTTGTACCCGGCTTCGGCCAGCAGTAGATCGGATCGAAGT  
CCACATATGTCCCATGGAATTCGCGCTGCTCCTGCGTCCAGATCTCGATTATCGCGCGCAACCGCTCATCGATCACAC  
GTCCGCGCACCGCAGGGTCCACACCATGGTTGGCGACTTCTTCGCGCA

## Clone Rv54

:::Rv54SP6.seq:::

ATACTCAAGCTTGTGCGGGTAAACCCGACGAGGGCGGTGGGTGCGGTGTCAAAAACAACCACACTTCTTTGCGGTTT  
GGTGATCTCGACACCGGCCGCGAGCCGACCAACCATGCGCGCGTAAATCGGCGATCAGCGCGTGGCTATCGCCTGGGT  
GCCGCCACCGGAATCGGCCAGCCGACCGAATGGGCCAGCGTTGCCAGCATCAGTCCGGCGCCGGCCGACACCACTGA  
CGGCAACGGTGAAATCGCGTGGGCGGCAACGCCGGTGAACAACGCGCGGGCATCTCGCCCGCCAGCGACCGCCAGGC  
AGGGGTGCCCTGGGCCAGCATCCGCGAGCCGAGACGCGAGGACCGAGCCAGTGCAGTAGGCAAAGACCGCTTGTGCGA  
GACATGAATCCACGACCGT

:::Rv54T7.seq:::

AGCTTATTGAACCGCGGGTCGCGAGGCAAAGTGGACCTCATAACGACTCGGGTCCAGCGACCGCGCCAACACGAACGGC  
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TTGGGCGCCGTGCTCGTCCAGCGTCCGGTCCCGGGTCGCCGCGACGCTTGTTCCTCCATACTCGCCCCCTAATCT  
CGAGGCGAGCCGTACCCGCGAGGCAACCTCCCAAAATGCAATCCCCCAAAATGCAATGCGTCGAGCTATTTCTCACAC  
CGACCGCTAGTTGCGGATCAGAAATCCGTTGGGCGCGGAAGTCCAGCCGAATTTGTTCTCCCGCTCCGCATCATGCTT  
GTAATCGTTTGAAATTCATCCTCATATGCCTCGATCGTTTCATAGGGTCCAGGCCAAACCGGGCA

## Clone Rv55

:::Rv55SP6.seq:::

CTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCC  
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CCAAACCGGGGCGACAGCTCCCAATTGACGTGAGCCCGCTCACTTGCTGGGTAAGCGTCG

:::Rv55T7.seq:::

TAGCGCCCCCTCCCGGGCGGAGCTCCACGGCGTGGATCAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGC  
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TCTCCCCATCGAGATAGTGGAGCAACGCAATCCGTGCGGTACGGTTCGGGTTCGTACTCGATGTGCGCGACCTTGGCGT  
TGACACCATCTTTGTCATTGCGGCGAAAGTCGATCATCCGGTAAGCGCGCTTATGACCGCCGCTTTGTGCCGGGTGG  
TAATCCGGCCATGCGCGTTGCGTCCACCGCGACCGTGCAGCGGGCGCACCGAGCGACTTCTCCGGGGTTGACCGGGTGA  
TCTCGGCGAAATCAGATACGCTGGCGCCGCGACGACCAAGCGTCGTGGGCTTGTCTTGCGAATTGCATGTCTAATCA  
GGTCTTTCTC

## Clone Rv56

:::Rv56SP6.seq:::

TGAAATATATAATACTCAAGCTTGCCAAAGAAGACCTCGTCGACCAAGCAGGACGCGACCGTCGAGGTGGCGATCCG  
GCTTGGCGTCGACCCGCGTAAGGCAAACAGATGGTTCGCGGCACGGTCAACCTGCCACACGGCACTGGTAAGACTGC  
CCGCGTCGCGGTATTCGCGGTTGGTGAAGGCGGATGCTGCCGTTGCCGCGGGGCGGATGTTGTCGGGAGTGACGA  
TCTGATCGAAAGGATTCAGGGCGGCTGGCTGGAATTCGATGCCGCGATCGCGACACCGGATCAGATGGCCAAAGTCGG  
TCGCATCGCTCGGGTGTGGGTCCGCGCGGCTGATGCCCAACCCGAAACCGGCACCGTCACCGCCGACGTGCGCAA  
GGCCGTCGCGGACATCAAGGGCGGCAAGATCAACTTCCGGGTTGACAAGCAGGCCAACCTGCACTTCTC

:::Rv56T7.seq:::

GCTGAGCTCCACGGCGTGGATCAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGATGTCGGC  
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GTGGAGCAACGCAATCCGTGCGGTACGGTTCGGGTTCGTACTCGATGTGCGCGACCTTGGCGTTGACACCATCTTTGTC  
ATTGCGGCGAAAGTCGATCATCCGGTAAGCGCGCTTATGACCGCCGCTTTGTGCCGGGTGGTAATCCGGCCATGCGC  
GTTGCGTCCACCGCGACCGTGCAGCGGGCGCACCGAGCGACTTCTCCGGGGTTGACCGGGTGATCTCGGCGAAATCAGA  
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## Clone Rv57

:::Rv57SP6.seq:::

ATACTCAAGCTTGTGGTGACCTCGCCGGCGAACAGTTCTCGCACGATTTCCGGATTAGCGGGACTGGTCACCAAGTTG  
GGTATGCGGGAAGGCGCTGACGTTCCGCCGCGATTAGCTGTTTGATGGACGCGGCGGTGATGTCCTGATCACGGAAGT  
GCTGTAATAGCCCAGGTCGCCACGCTTCCATCCGGGCCCCGACCCGGC

:::Rv57T7.seq:::

GATGATCGCCGGTGCCACCCCGATCCGTGCCTCGGTGACGCGAACGTGCTTTCCGGTCCGGCGACCACCATGTCGCA  
CGCACCAGCAGGCGCAACCCGCCGCGCCGACATGCCCGTTGATGGCGCCGACCACCGGCAGCGGCGACTCGACGAT  
GGCGCGCAACAGCGCCGTCATTTCCCGCGCCCGCGCCACCGCCATCCGGTACGGATCACCACCACCTCCGCCGGCCTC  
GCTGAGGTCC

## Clone Rv58

:::Rv58SP6.seq:::

ATACTCAAGCTTGCCGCAATCGAAACCAACCTGTTTGTGCCGCAAGAAATTACGCCGTGGCCCGGCGCCGATCAAGAA  
ACGCCCCGGCGCGCGGGTGTCTGTCGATGGCATGACGGGCACCAATGTGCACGCCATTGTGAGCAGGCACCGGTG  
CCAGCCCCGAATCCGGTGCACCAGGCGACACCCCGGCCACCCCGGTATCGACGGCGCGCTGCTGTTCCGCGCTGTCG  
GCCAGCTCGCAGGACGCGCTGCGGCAAACCGCCGCGCGGTGGCCGATTGGGTCT

:::Rv58T7.seq:::

TTGGCGGGTTGGCCACANCANCCCGCGGTGACGGCGACGATGCTGGGCTGGTTGGCGCCCTGCGCCACCGCGGCTTG  
CATGCTGGTTGGCTGTCTTGGGACGATCCCGAAATAGTCCACGCGGATCTGGTGATTTTGGGGCTACCCGCGATTAC  
CCCGCGCGGCTCGACGAGTTTTTGGCCTGGACTACCCGCGTGGCCAATCTGCTGAAGTCCGCGCCGGTGGTGGCCTGG  
AATGTCCANCGCGTTACCTACGTGACCTTGATGGGATCCGGGGNT

## Clone Rv59

:::Rv59SP6.seq:::

NCGTGGACACCGGTGTGCANCGCCACCAGCCGCATGTCTGCANGTCNATTCCGTCTCGGCAACATCTTGAATGCCGA  
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CGGCGGACGGCTCGACGAGCTGGAACCTCAGCGACGACGATCCGGAATTGATCACCAGCACGGTGCTACTCATGGACC  
CCTGCGCCTGAATCCCGTGATGGCCACGGTGTGACTATTTCGTGACAGTGACCCCGAGATAGTCTTACGGCTGCGT

:::Rv59T7.seq:::

CATGTATTGCCGTGCTCACGGCGCCACGCTCGATGGTTTCTCGAAGTCTCCGGGCTGGTGTACAGCTTCTCGTTGATC  
TCGTTCCGCCACGCCGTCTCTTCCCGCCGACGACCCGATCTCGATCTCCANAATGATCTTGGCGGCCGCCCGCCGCTT  
GAGCAGCTCCTGGGCGATGGCCAGGTTCTCATCGATGGGCACTGCCGACCGTCCACATGTGCGACGGAACAAAGATG  
TCACCTTGCTCACGCGTGCGCNAGATCNCANAAGGGCCGGACATACTGTCNACTTGTCCTTGGGCAGTGGTCCGTGTC  
AGCCACGTGACGGGTACTTGGCGCGATAACGTGGT

## Clone Rv5

:::Rv5SP6.seq:::

GCCACCACGACCCGGCCGTAAGTCTGCTCACGGAAATGCGGCCAGGCGCGCGTAGCACGTGGTATCCGCCATAAAGG  
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ACCACACCGTGACGGCGCCGAATTCGTCAAGCGCGGTCTTGATGATGTTGCTGCGCCGTCTCGGTGGCGACGCTG  
TCCTTAGTTGGCGACCGCCCGCCCTTGTGCGCAATCTCGGCGACGACCTCATCGCCATCGCCGAACGGCGCCC  
GTGCCCGTGCGGGCGCCACCGAGGTGCTTGACCACGA

:::Rv5T7.seq:::

CAGGCATGCAACCTTTGTCCACACGGCGTCTACTCCGTGCAAGGTCCGACCGCTTCCACGTCCCGCCGTGACGGTGCT  
CCATCTCCCTCAGCAACGCGTGAAGTGGTCCGATCCCGCGGCTTCAGG

## Clone Rv60

:::Rv60SP6.seq:::

GTTGAGACGCAACCAGCGCACACGACGATTTGGCGTAGCGGCGGACGTCTGCTCGATTCGATCACGTGCGGCTCGCA  
TCGAGCATGGCCCGCGACGCTACACGATCGCCGTCGTCGATGACACGACCGAGCCGTACGCCGGCCGTAAGCCGCGCC  
AGGATTCGGCGAAAAACGTCTACGTGGCGGGTGTACTGGGTGTGCAATGATTGCTGGGTGCGTATGCGTCTTGCAAT  
CGTCGACATAGATCCGTGCGCGCATCGGTGCAAACTCCGGGTGAGTGGAATACACTTGCCGATCACGCGACGTGCG

CGGATCGATGCCGACCGAAATACGACCACATGGCTCTTGTTGCNCAGTGTTGGCGGCATCAAATACCCTCAGTGCCGT  
CCGAC

::::::::::Rv60T7.seq::::::::::

TTNCCGCCTTNACGCCTACTCCNAGACGATGCTCGACGCGTGTGAGCACACGGCGCTGCTGTAGACGGCACGGCGCAG  
CTGGATCGCGCTTGGTGCACCAAGCCTCTACGCGCGTTCGCTGCGTCATCGGGTACCGAACATATCCGGTCGTT  
GCGCAGAGTGTGCATGTGCGGCTCTTGTGAACGAACATAGCAAAGCGTATATGTCTGTGGCGGCTCTGCAGATATCGC  
GATAATACGTATATACATAAGGTGGCGCGCATCTATCGGTATATCCGTTATGGCGGACGTGCGTGAGCGTGAGTCGC  
GGCGCATCGCGCACTTCGCGATCGCGTGACTGGTCCTCGCGACTGCGCGCATGCGTAGC

Clone Rv61

::::::::::Rv61SP6.seq::::::::::

GGTGATGACGCATTGCTTCGAATGAGTCATTGACTACTCCCGTGTTGTCCTGCGATGGTGGAGTGCCGCGCAGCCT  
TGCCCGANGTCGCGATCGCGTCGCGGGCTTCGGGGAGCAGACTGACCTGCAGATGGAAGTCGTGCCACATGCCCGCGA  
ACGGCGAGCTCGATGCTTGTTCGAAGNGCGCANGCGGTTTCGATCTTGTCCGCGTCAACGCAGATCGGATCTCGCC  
GCGGTCTGCATGACGATGGGCGCAGGCCGCTCATGTCCCGTAGACGGGGAGATACGGGCAGCCGCGGATCGAGACCT  
ACGTAGCGCGGGCGCCATCGTGCCATCGACGAAGAATGACGGATCGCGCAGCGCCGTGCGCTCGCTTCGATGTCACGC  
GAGATCGCCACGGCAGATCAGCGATGCGCGGGC

::::::::::Rv61T7.seq::::::::::

CGGTACGCCGGCAACAAACGCCTTGTGACGAGCGCGTCCGAGCGGTTCATCGGCCTCCACCGTCATGCACAGCTCCTTC  
TCCAGGTCTACGCCGACGTGCGGGTCCACATTGGTGAGCTTGGCGAATGCCTCGGCAACCTCGTCGAAATGCGCCTCC  
GCGTCCGCATCGAAGGTGCGCATGTCAAAGATCAACTCGACGTAGTAGCTAGTTACCGCATCAGGTCAGTGTTCGCTG  
GCCTCGGAGTCCGGCCGAACAATGGCCATTTCGCGGACTCTAGAATCCAGTCATCGTCTCGGTGACGACGCCTTGCC  
GATCAGATAGCTCGACCGGATCGGAGAGAATCTGGTTCTCGT

Clone Rv62

::::::::::Rv62SP6.seq::::::::::

ATACTCAAGCTTAAGCGCAGCAGTACCGGCGGTGCCTGGGCATCCCAGCAAAACGGGGAGCTCAACGAACGATTCTTG  
AACGAAGGGTCGTCCACCAACCTCCAAACCGAACGGTTGCCAGCCCCGGC

::::::::::Rv62T7.seq::::::::::

GCAAGTCCGCTCAATGTGGTTGTGATCACANGACTACGTGCGCTCAATCAGCTCAAACGTCACCCCGTGGCGTGCTGC  
GCAGCATGAAGGTGCGCGCCCCGCACGATGTGGGCGAAGCAACAGGTAATAACTGGTCGGCATGGGTCAACCCTCATTG  
GGCCGTTGCGGATCGGGTGACGCCCCGAGTGCCGGTCAACTCAACACCGCCTTACCGATCTTTTCGTGAAAATG  
GCGGTGCTGTCGGGTATACGTCCGCGATCCACGAGGCGGAATCCGCTGAGCCGCACTGA

Clone Rv63

::::::::::Rv63SP6.seq::::::::::

ATACTCAAGCTTCGCGCCCTCAAGCGGCTGAAGGTGGTTCGGGCGTNCCAACNGTCGGGCAACTCGCCGATGGGCATG  
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GACTTGAACGACCTGTACCGCAGGGTGATCAACCGCNACNNNGNTGAAAAGGCTGATCGATCTGGGTGCGCCGGAA  
ATCATCGTCAACAACNAGAANCAGGATGCTGCNNGAATCCGTGGACGCGCTGTTTCGACAATGGCCGCCGCGGCGGGCC  
GTCACCGGGCCGGGCAACCGTCCGCTCAAGTCGCTTTCGATCTGCTCA

::::::::::Rv63T7.seq::::::::::

TGCGCATGGCAGTTGTTGCCGGCTTGAGTCGCGTTAGCGCGGATTCACACATCCCTTGCGAAGTCGTGGGTGCAAT  
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GGCGTTGACACCATCTTTGTCATTGCGGCGAAGTCGATCATCCGTAAGCGCGCTTATCGACGCCGCCCTCTGTGCCGG  
GTGGTAATCCGGCCATGCGCTTTCGTCCACCGCGACGTGCAGCGGGCGCACACCGACTTCTCCGGGTGACGGGTGATC  
TCGGCGAATCAGAACCTGGCGCGCGACACAGCGTCGTGGCTGTACTTG

Clone Rv64

::::::::::Rv64SP6.seq::::::::::

TGGGTGATCAGATACTGGCTAGTTGGTCGGGTGGGGTGATCGAAGATCGCGGTGGCCGGCAGCGTTACTGCGGTGACG  
CTGTTAAGCGGTTACGTACTCCACGGCACTCAANGAATTANATCCCGAATCGGCAAACCTGGCCAGCGTCGAGTCCG  
CAGCGCGCTGCGCCCCCACCCTGCGGCATGCTCACATAACACCTCGATCGCTGCGGGAGTTGCTCGTCGGCCGAC  
CGACCGGCCAGCCGGGCGGCAACCGGAGGACCAAGATTACGACACCACCATCGCTAGCCCGATCTGGCCGCGCGTGG

.....:Rv64T7.seq:.....:

TCGTAGCGGTTGCGACCAANTCCGCGGACAGCTCCGCCACGCGACGGGTGCGGATCACCGCGGTCAAACCACCGAGCGG  
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GCGCTGGATGTGTTGTGCCGCAACGGAATCCCACCTCAATTATGACCTCGTTGTGGGCGAGCGCGGTATCGTACGCCC  
GACCAGGAATCGTCGATGCTATCTCACGTACCGAAGGCCTCTCCCAGCACACCGCATCCAGAACGTGCACACNGTCG  
ACATGTCTCGGCGGATCCGCCTGCAGAACGAACGCCANGTGCCTGTGCGACACGGGTGCGGATCACCGCTCGCACGC  
GGAGATCGGCACACGCGCAGCGCATCGATCATAATCTCTCGATGCGGTCTCCACCACCGAACAG

Clone Rv65

.....:Rv65SP6.seq:.....:

ATACTCAAGCTTCGCTGAGGTGGTGGGGCACGATCACGTCACCGCACCGCTGTGCGTGGCGCTGGATGCCGGCCGGAT  
CAACCACGCGTACCTGTTCTCTGGGCCGCGTGGCTGCGGAAAGACGTGCTCAGCGCGTATCCTGGCNCGGTCTGTGAA  
CTGTGCGCAGGGCCCTACCGCCAAACCGTGGCGGGTCTGCGAATCCTGCGTTTCGTTGGCGCCCAACGCCCCCGGAG  
CATCGACGTGGTAGAGCTGGATGCCGCCAGCCACGGCGCGGTGGACGACACCCGCGAGCTCGGGACCGCGCGTTCTA  
TGCGCCGGTCCACTCACGCTACCGGGTATTTATCGTCGACGAGGCGCACATGGT

.....:Rv65T7.seq:.....:

GCACTCACGCTGGTACAAGACCTTCACAAAATCTGAAATCCTGACCCGATACTTGAACCTGGTCTCGTTCCGGCAATAA  
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GCTGGCCGGCATGGTGAATCGACGACGCTCAACCGTACACCAACCCCGACGGCGCGCTGGCCCGCGGGAACGT  
GGTCTCGACACCATGATCGAGAACCTTCCCGGGAGGCGGAGGCGTTGCGTGCCGCCAAGGCCGATCCGCTGGGGT  
ACTGCCGAGCCCAATGAGTTGCCGCGCGGCTGCATCGCGGCCGGCGACCG

Clone Rv66

.....:Rv66SP6.seq:.....:

ATACTCAAGCTTGTATAAAAGATCGGTGAGCGCATCGATTGCTCCGCCGGGTTTGCCGCTGCGGCGGCGGAGCTGC  
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GCGTTACTGCGGTGACGGCTGTTAAGCGGTTACGTACCTCCACGGCACTCAAGGAATTAAATCCCGAATCGGCAAACG  
CCTGGCCAGCGTCGAATCCGGCAGCGCGTTCGCGCCCCAGCACCGCTGCGGCATGCTCACATACCACCTCCATCGCTG  
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.....:Rv66T7.seq:.....:

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AATTGTGCGGTTCCGCGCAACGGTGAGGTGCTGGTCNGCCAGCCCGCCAAGAACAGGCAGTGACCAACGTGATCGC  
ACCGTGCGCTCGGTCAAGCGACCATGGGCAGCGACTGGTCCATAGAGATTGACGCAAGAAATACACGCCCCGAGATCT  
CGCCGCAATTCTGATGAAGTGAACGCGACCCGAGGCTACTCGGTGANGACATNACGACGCGTTATCACACCCCGCCTNC  
TTCAATGACCCACGTCNGGCACCAAGGACCCGGCAATCGCGGCTCACTTGNGCGATNGTCNACAACCAACGCGNCGC  
CTGGCTACGGGCTCAACAAGGCANAAGACACAATCCGCTCTCGATTGGTG

Clone Rv67

.....:Rv67SP6.seq:.....:

ATACTCAAGCTTATCGAGGCGGCGCATACCGAAGCGTGGGAAATCCAGACCGAATACCGCGACGTGCTGGACACTTTG  
GCCGGCGAGCTGCTGGAAAAGGAGACCTGCAACCGACCCGAGCTGGAAAGCATCTTCGCTGACGTGCAAAAAGCGGCCG  
CGGCTCACCATGTTGCACTTTCGTTGGCGCGGATCCCGTGGACAAACCGCCCATCAAGACACCCGGCGAGCTCGCG  
ATCGAACGCGGCGAACCTTGGCCCCAGCCGCTCCCCGAGCCGGCGTTCAAGGCGGCGATTGCGCATGCTACCCAAGCC  
GCTGAGGCCGCCCGGTCCGACCCGGCCAAACCGGGCACGGCGCCAACGGTTCGCCCGCCGGCACCAACCGGTCCGGTGA  
CCGCAGTACGGTCCCCCAGCCTGACTACCGTGCCCCGGCGGGCT

.....:Rv67T7.seq:.....:

TGGCCGGGCTGGTAGCCCGCTATGGCAAGGTTCCGCTCAATGTGGTTGTGATGCAGCAGGACTACGTTGCGCTCAAT  
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AAGAACCTGGTCGGCATGGTTCGAGCCCTATTGGGCGGTTGCGGATCGGGTTGCAGCGCGCCGAGTGCCGGTCGAA  
CTCAACACCGCCTTCACCGATCTTTTCGTGCAAAATGGCGTCGTGTCCGGGGTATACGTCGCGGATTCACACGAGGCG  
GAATCCGCTGAGCCGCGAGTGATCCGGGCTCGCCGCGGCGTGATCCTGGCCTGTGGTGGTTTCGAGCATAACGAGCAG  
ATGCGAAT

## Clone Rv68

:::Rv68SP6.seq:::

GTCCAGTCAAGCATCGGTCTCTCCGACTACGCCAAGANTGGCGACGTGTAGTGCANACAGCGGANATGGTGGCGCC  
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GTCAGCCGCATCCACTGGATGCCTTCTCGGNGTTTCAATCANGTACANGCGACGTTTCGCCACCATCGTGCCGGGGCAC  
GGTTAGCGAGAAACCGCGACTTCACCGATTGCCTCGGTGATGCCGTGGAACAGATCGGGCCTATTGTCGACAGCCAG  
TGTGATNCGTATTTGCCGCGGTGCTCCTCGTCGCAACGATGCGAACACAGATCCGTGGNGGACGATAGCGGCTGACAA  
NGTGGGGGCAACAATCACATGCCACATTTCTTCATTTACGCCCAACAACCAGACTTCGTCTCGATGNGCCG

:::Rv68T7.seq:::

CACGCGGTCTGGCCCGATCCGAAGATCCCTTTGCCGGCGTGGCGGCTCTGCTCGGCGGTGTTGTACACTTCTCGAACA  
CCTCGGCACCGACACCACCACCGTNGCTTGAACACCGCCAACATCGGCAGCAGATCTTGATGGTCCTGGTGAATCCCA  
CGGTGACTTTGGAGTGGAAGGCGCCATACTGATCGCCGCGCCAGCACATGAGCTAGCGGCAGGAAAACCAGCAGCCGC  
TCACCTTGCGCAGCAGCGTCNGGTGATATGCCTGGCGCCCTTAATCTCGTGAACCAAGTTGGATTGGGTCAACTGGCAG  
CCTTGGGTCTCCGGTGGTGCCGANGTGTANATAAGCTCCCGGGTCCGTCAACGTANTGCGCAGGCGGGGTTACTCGG  
CGGGTCAACGAGCCCCGCTCGTGAGCNATCAGCCTTTGGACCGAACGGGATTCTACTCCGAGGCGGCCCTCCGAAA  
TCGGCACATGTCCTTTGATCGTTCGCAACAN

## Clone Rv69

:::Rv69T7D3.seq:::

GGCCATGTACATCGGTGGTACAGGTAAACCGCGCCGTGTGCGCGGTCTCGGAGATCAGAACGTGGTTCGAGTTGAAC  
CGCGGGCTTTAGCCAGTCGCGATAATCGGCGGAAGTTCGGCGCCTGCCGCCCCAACTAGCGCGACTCGCCACCTAGCA  
CACCGATGGCGAAGGCCATGNTCCGGCCACGCCGCCGCGGTGCATCACCAAGTCATCGACTAGGAAGCTAAGCGACA  
NCTTGTGCAGGTGTTTCGGGCAGTAGCTGCTCGGAAAAATCGGCTGGAAACCGCATCAAATGGTTCGCTCCAATCGAACCG  
GTTACCCGATCGTCACAAAAATCTCCGTCCT

## Clone Rv6

:::Rv6SP6.seq:::

GGGTCTACAACCACCGGTCTGACTTCTGGGCTTCCACCGCTCGCGCCGTTCGCGACAAACAGCGCGGTTCGAACCGACA  
CTCGTTGTGATGTCCCAGCTATCACCTCCGGTAGGCACCCAATCGACCCTACCCGGCTATCTACCCCCGATCTCCAG  
GCTCCGCCGATCCATGCGCATCCCGGTCCGGATCCC

:::Rv6T7.seq:::

CAGGCATGCAAGCTTGTGCTATTCCGTGGCACTGTCAGACATATGCGCCGCTCCTCCTCATCGCTGCGCTCGGCATCG  
TCGCCGGCGGTTCATGGCGTCACCTACCCAAGCCGAACGCGAAACGAGAACGTGTTCCATTATTAGGGTGTGAGCACC  
AATACCAGATTGCTCACCAGGAACCTACGCGAGCACCGGGACGGATGTCAGCCACCACGCCCATCTGGGGTGGTAGCGG  
GGAAATACGGCTAACGCGGCTCCGGTGCCGGCAGCCCAGCGCAGACCCTCGGCGGCGGACACGGCTAACAAACGACGAC  
CCATAGTTGTTCTTTGCCGGATGGCCGTGTTTGCTGACATATCGGGCGCGGCGCGCGCGCGCC

## Clone Rv70

:::Rv70SP6D2.seq:::

NCTACGCTGCTGAATGTTGTGCGCCGGAGGANCTCAAGACCCACGCGGTTGTACGCGGACNTGCGACATGTTCAACCG  
CCGGA

:::Rv70T7D3.seq:::

CTAACCAACAAGCCATGGTGGTTGGCGCCGTGAGAGGTGGCGGTCGCCACAACGGGAAGATCGCCTTGAGCGTCGC  
TCGACCGCCGCTCGAGTTGGGTGATAACGAAGTACTGATGCCGATCATGTGACGTGTCCGTGCGATCAGCGTGCAG  
CGGCGACCCCTCGACGAGCCTCGGTGCCGCGCGGCCAGGGCACCAGCTGTTTTAGCGCATGTGCTCCGCCGGTAAT  
AAAGGANGTCGGTTCGCTCCGCTGCTGTGGTTGCGGAATAACATCTTCCCTTCTGCAACAGGATGAGAATGGTTTAA  
ATTGCTC

## Clone Rv71

:::Rv71SP6.seq:::

CTAAGCTTTCGGGTCCGCCGCCACTAGTACCGGTTGCCGGCCCCCGCGACCTAGAATGTTCCGCCCATTCGCCGTTTC  
CTCCCGCCCGCGGTT

.....Rv71T7.seq:.....

TCTGGTGCCGGGTGTGCCGACGGGTCCGTCCGCCTTGCTTCAGTGATTCTGTGATGCGACCGGCAACGTCTCTCGTTG  
TTCGGTGTCTATGTGGTCCGTCTCTCCTTGTTCCGCATACGATT

Clone Rv72

.....Rv72SP6D2.seq:.....

GCGATCGNTNACCACAAGGGCGCAACCGTTCCGCGCTCGACTGAACGTGCTGCCGCCTGGAGAACTGGCGCTGCTGCC  
ACCTGGTCCGGCGCATCGGCACCTTCGAGGACTGGATTTCGACGCGTGGCCCCGACCTGANGTNGGCGGTGGACNNGTGTG  
CACCCGGTTGATTCTCGGCCTTGCCGGGATGCCACCTGCGCCTGGTGGTTCGAT

.....Rv72T7D3.seq:.....

CGTGACCGGACGGGGTGCCGCGCAACCGGTCTTGCCCAATTGCCGGGGACTGGGGCTGGAGTATAAAGCGGGCCTGT  
TGCCGGAAGATAAAGTCAAAGCGGTGACCGAGCTGAATCAACATGCGCCGCTGGCGATGGTGGTGACGGTATTAACG  
ACCGCCAGCGATGAAAGCTGCCGCCATCGGGATTGCAATGGGTAGCGGCACAGACTGGCGCTGGAAACCGCCGACGCA  
CATTAACCATAAACACCTGCGCGGCTGGTGCAAATGATTGAACCTGGCACGNCCACTCACGCCAATATCCGCCAGAACA  
TCACTATTGCGCTGGG

Clone Rv73

.....Rv73SP6.seq:.....

ATACTCAAGCTTCTTACCCANAGCATGAACCCCGCCGTCCAATGCCGCCACCGTGGTGCTGTGCGCCGGCCGGGTGCG  
GGCACAATCGCCGAGTTCGGCGAACAGATCCTCGAAGGTCTTCACGGCCAGCGATTGTTGCACGTGTGAGCCAGCCAA  
GTCACGGTGGTTTGACGCCACACGTTCCGCCACCGCCGCGCCGCGCATTAGGGCATCCTAATATAGGTTAGGCTACCT  
ANTTATTCTGTGGTCNAAGGAGGACGCCAACGTGACCTCCCGATGTGGTTCGCAGTTCGCCCGGAAGTGCCGTCA  
GCATGGCTGTCCACCGGCATGGGCCCCGGTCCGCTGCTGGCCGCGCCAGGGCGTGGCACGCGCTGGCCGCGCAATAC  
ACCGAAATTGCAACGGAACCTCGAAGCGTGCTCGCTGCGGTGCAGGCAACTCGTGGCAGGGGGCCAGCGCCGACGGTT  
CGTCNTCCCCATCAACCGTTCCGTATTGGCTAACACCTGCACGGTGGCACCGCACAACGCCGCCACAACGCGCCCC  
GGTATAC

.....Rv73T7.seq:.....

GGCCGAACCTAATCGGTTGTTGGCGGCTGCCGAGTTGGGTCACTCGGGGGGTGTGCACTGGCACATGGTGGGCCGGAT  
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GCTGGATCGGGCGGTTGTTGCGGCGCTGGCCGAACACCGTCTGGCGAGCGGCTGCGGGTTTACGTCCAGGTGAGCCT  
CGACGGTGACGGATCCCGGGGCGGCGTGCACAGCACGACGCCCGGCGCCGTAGACCGGATTTGCGCGCAGGTGCAGGA  
GTCAGAGGGCCTCGAAGTGGTTCGGGTTGATGGGCATTCCGCCGCTGGATTGGGACCGACGAAGCCTTTGACCGGCTG  
CAATCGGAGCACAACCGGGTGGTGGATGTTCCCGCACGCGATCGGTCTGTGCGGGGCATGTCCAACAACCTTGAAAT  
CCCGTCAACATGGTTCGAC

Clone Rv74

.....Rv74SP6.seq:.....

GCTTCCCTGATACTCGACAGCCCCACTCGGGCCAATACGTGAATGTCCTAGCATTTTTCACCCGTTACAGGGCTAG  
TCGAGTAGTAGACGATTGATTAGCCTGAACGTACCTCCGACGGCCAGCTGACGAACGGGTTTGACGGA

.....Rv74T7D3.seq:.....

TCAGCTGTCTGTAGAAGGGCTGGCGATACTGTGCACTGTCTGATATCGCNNCGTNGTGGGACTATNCAGNCCATNANG  
ATGCGGTTTCNGNNNTGCAGAGNATCCTGGNACACATNCGGTTACGTTAATCANCATCGCGANTTNCTNCGTNTTCG  
ATTANTTCTGCTAACGNNTCTNNNAGTGCCTGCGGGTTCGACTCTAGAG

Clone Rv75

.....Rv75SP6D2.seq:.....

NCTCTGCCGGGNCAGAGCGCAGAGTCGGACGGCTTCGTGATCGTGAAGCGACCNTGCGATGANCAGATATCGNTNAC  
ACTGCTCANAACTTCGGATCATCGNTGATACACAGGCCAACGGGTAGCGGTTGTCCAACCGCTTCGTCAACGANATG  
GGATCGTGACGANCTACGCTCGCAGGATATGTCGCGNACCNGNTCTAGANAN

.....Rv75T7D3.seq:.....

CACCTTCATGCTCGTGGCTGGCCTGATTGTCNCGAGNGGTTAGCTCCTCGAGTNGTGACGTATCACTCCGGCNGAC  
TANCCGTATCNGCGTCCCGCACCGGTCAACTGGTCTAGCCACACCGGGGAGAATNCNCGACCGGNGCTATCGACCNAT  
CACGGCTTGTCGNNAGATAGNCAGCC

## Clone Rv76

:::Rv76SP6.seq:::

ATACTCAAGCTTGCCAACCGCCACCCTGCATCCGGGGGGCGAGCACTGCTCCGCCGACCAGTACGAACCAACCTGCGG  
TGCCAGGCCATTGACAATGTGCTGGTCGGCGCCCCGCGAGTTCTAGCACAGCAACGCCGCGGCCACCACAGGGGCG

:::Rv76T7.seq:::

CGGTCGGTGTGCTTGGCGGCGTCGGTATCAACACCGCCCCACGAAATGGGGCACAAGAAGGATTGCTGGAGCGGTGGC  
TGTTCAAGATCACCTCGCCAGACCTGCTACGGGCACTTCTACATCGAGCACAACCGTGGCCATCACGTCCGGGTGT  
CCACACCGGAAGACCGGCGTCGGCGCGGTTCCGGCAAACCTTTGTGGGATTTCCCGCCCCC

## Clone Rv77

:::Rv77SP6.seq:::

AATACTCAAGCTTCGCGGAGGTGGTGGGGCAGGAGCAGTCACCGCGCCGCTGTCGGTGGCGCTGGATGCCGGCCGGA  
TCAACCACGCGTACCTGTTCTCTGGGCCGCGTGGCTGCGGAAAGACGTCGTGAGCGCGTATCCTGGCGCGGTGCTTGA  
ACTGTGCGCAGGGCCCTACCGCCAACCCGTGCGGGGTCTGCGAATCCTGCGTTTCGTTGGCGCCCAACGCCCCCGGCA  
GCATCGACGTGGTAGAGCTGGATGCCGCCAGCCACGGCGGCGTGGAGCAACCCCGCGAGCTGCGGGACCGCCC

:::Rv77T7.seq:::

GATGGCACTCAGCTGGACAAGACCTTCACAAAATCTGAAATCCTGACCCGATACTTGAACCTGGTCTCGTTTCGGCAA  
TAACTCGTTTCGGCGTGCAGGACGCGGCGCAAACGTACTTCGGCATCAACGCGTCCGACCTGAAATTGGCAGCAAACCG  
GCGCTGCTGGGCGGGCATGGTGCAATCCGAACAAGCACGCTCAACCCGTACACCAACCCCGAAGGGCCGCTGGCCCCG  
GCGGAACCTTGTCTCCA

## Clone Rv78

:::Rv78SP6.seq:::

AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCTGGGCGTCGTGGTGCCC  
GGCCTGCCGGTGACGAACTGGATTTTACTGCCATCTCTCGCGACCTGAGGTGGTCCAGGCTTACAACACCGACCCA  
CTCGTGACCACGGACGGGTTCCGGCCGGGATTGGCCGCGCGCTGCTGCANGTGGGCGAGACCATGCCGCGGCGANCA  
CCGGCATTGACCGCGCCGCTGCTAGTGCTGCACGGCACCGATGACCGGCTGATCCCCATCGAAGGCAGCCGTGCGCTG  
GTCNAATGTNTNGGATCNGCCGACGTGCANCTGAANGANTATCCCCGGCTGTNCCACNAGGTGTTCAACGAACCGGAN  
CGCAACCAAGTG

:::Rv78T7.seq:::

CAAGGCATACGCCAAGACCCAAGGGATCGCAGTCACCTCCGTCAACGGCCTGGTCGCCGGCCACGGGTCCGTGCAGGA  
GACGTGGCTGGCCATGCAAAGCGCCGCCCTTATCAGGAACGCCCGGCTTGTGCGCTTTTCTGTCATCGACACATT  
TCCGGAGGTGTTGTGTTGGCGCANCGCGGAGACAGGCCTGGGATGGCGTGCATCGTATCGGGAATGCGATGGC  
AACACTGAACTACGAGCGCATCCTGCGCCAGCATGACTGTTTCGACTACGTCGTCGTTGGCGACGGGGANGTAGCGTT  
CACCAAGCTGGCCTTGGCCCTGGCGAATGACCTGCGGTTGACGACTCCCGGGACTAACCCGCCGTANTGAGCAAGGAC  
AGATTCTGCGCACACCTCCTCGCTGGTCGACCTTGACA

## Clone Rv79

:::Rv79SP6.seq:::

AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGCCGGTGATCTGGGTGGC  
CACTCGGCGGGCACCATCTCCATCACGACNGCAAACGCTCCGGCTTCGGCGACAGCGATCGCGTCTGCGATNGTTTG  
TTCGGCGGCGTCTCCGCGGCCCTGCACCCGGAAGCCGCCAAGGTGTTGACNCTTTGCGGGGTGAAGCCGATGTGTGC  
CATCACCGGGATNCCCGCCGCGGTGACACANGCGATTTGCTCGGCCACCCGCTCACCGCCCTCGANCTTGACNGCATG  
TGCGCCGCGCTCCTTGAAGAAACCGGTGGCGGNGGCAACCC

:::Rv79T7.seq:::

CGTTGAGATCCAGCTGCGCACTGTGCAGCGCCTCGGTGGTCTGCTCGGCCTGCCGGGATAACTCGTTGAGCTTGGCCA  
GCGCGTCGTCGGCCGGATCAGCCAGCACATTCGCGGCCAGGACGCCGAGGAGACGGTGAAGCTCGCAAAGAAACCTA  
TGGCGGACCGCATGATTACACGCGGATCAACCACCTCTGGTCGAGCCTCAAATTTGCTTCTTAAACGGGCCATCG  
ACGGATGACGTCGAGCTGGTTTAGGTCTCAAACAGGTTACGAAACGATCTCGGAATTGTCCAAAAGGGGAAGTTAAGA  
AAATGGATAGATTTCTACCATTTGCTGTGGACGATCGTACTTCTGCTATAGGGCTCCAGGGGCATCGACACGCAACG  
ACCTTACGCGACACCGGATCCGCGCTGGCGGCGGAACGGCACCANCGCAACCGAAGGGCCAATCCGACATCGG

## Clone Rv7

:::Rv7SP6.seq:::

ATACTCAAGCTTATCTAGGCGCCAGCTTGATTGGTCTGGTTGCATTGGCCAGCTGCGCGAGCCTGGCTCACTTCAACT  
ACAACAACCGCAAACAATTGCCGCCCTTCGGATCCGAGTTCGGTTGGGTACGCGGCAATGGANCACCATTTCTCGGTGA  
ATCAGACTATTCTGAGTACTTGATCATCCACTCTGCACACGACCTGCGAACCCCGCGCGGCCCTTGCCGACCTGGAGC  
AGCTGGCGCAACGTGTGAGCCANATCCCAGGCGTTGCCATGGTTTCGCGGTGTGACCCGGCCAAACGGGGAAACCCTTG  
AACAGGCCCCGGGCGACATACCAAGCCGGCCAAGTTGGCAACCGGCTGGGCGGCGCGTCGCGAATGATCGATGAGCGCA  
CCGGCGACCTGAATCGGCTGGCATCGGCTGCCAACCTGTTGGCCGACAATCTCGGTGACTTCGCGGTCAAGTCAGCCG  
GGCCGTTGCGGGTGTCCGACGCTTGTCCAGCCCCTCGCTTACTCCA

:::Rv7T7.seq:::

CAGGCATGCAAGCTTTTTGAGCGTCGCGCGGGGCGAGCTTCGCCGGCAATTCTACTAGCGAGAAGTCTGGCCCGATACG  
GATCTGACCGAAGTCGCTGCGGTGCAGCCACCCTCATTGGCGATGGCGCCGACGATGGCGCCTGGACCGATCTTGTC  
CCGCTTGCCGACGGCGACGCGGTAGGTGGTCAAGTCCGGTCTACGCTTGGGCCTTTGCGGACGGTCCCAGCGTGGTC  
GCGGTTGCGCCGCGAAAGCGGCGGCTCGGCTCGGATCAGGAATGCCTCACCGCCGCGGCACTGCACGGCCAGTGCCCG  
CGGCGATTGAGCCATCGGGACATCATGCTCGCTTCATACTCCTCGACCAGTCGGCGGAACAGCTCGATTCCCGGAACG  
CCCACGCATGGTG

## Clone Rv80

:::Rv80SP6.seq:::

AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGTAGAAAAGATCGGTGA  
GCGCATCGATTGCTCCGCCGGGTTTGCCGCTGCGGCGGCGGAGCTGCCGTGACCGTCTATTTGGGTGATCAGATACT  
GGGCTAGTTGCGTGGGTTGGGTGATCGAAGATCGCGGTGGCCGGCAGCGTTACTGCGGTGACAGCTGTTAAGCGGT  
TACGTATCTCCACGGCACTCAAGGAATTAAATCCCGAATCGGCAAACGCCTGGCCAGCGTCNAGTCCGGCAGCGCCGT  
CNCGCCCCAGCACCGCTGCGGCATGCTCACATACCACCTCGATCGCTGCGGCGANTTGCTCGTCNGCCGACCGACCGG  
CCANCCGGGCGGCAAACCCNGAAGACCCCAAGAATTCATCACCACCATCGCTAGC

:::Rv80T7.seq:::

CCTTCTTGACACCCACCTCGCCATCGACCTTGAGCACTCCGTGCTAGTTGGTGAACATGTGACCGGCGATCGGGCGGG  
TGAACGCGTACTGGGTGTCGGTGTGACGTTTCACTTACCACGCCGTAGCGCAGCGCCTCCTCGATCTCCGACTTAA  
GCGAACCCGAGCCGCCGTGGAACACGAAATCNAACGGCTTGGCGTCNGCCGGCAGTCCGAGCTTGGCCGCCGCCACCT  
GTTGCCCTTGCGCAAGGATGTCNGGGCGAANCTTGACGTTGCCGGGCTTGTANACGCCATGCACGTTGCCGAACGTCN  
CGGCCAGCANGTATTTGCCGTGCTCACCGGCGCCCANCGCCTCGATGGTTTTCTCGAAGTCTCCGGGCTGGTGTACA  
GCTTCTCGTTGATCTCGTTCGCCACGCCGTCTCTTCGCCGCCGACG

## Clone Rv81

:::Rv81SP6.seq:::

AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGGAAAGGAGATCCCCGGG  
AACCTGGTGGCAACCCGCCATTGGGGTTGTTGGGATTGCCGATCAGCGTGAANGAAAGCTCGTCTGGAGACAGCGGG  
TCGGCCGAAGCCGCAAGATTGGCCATCACTAGTGACGANATCGTGGCGCTCTGCGAGTANCCNAAGACAGTGACGTTG  
TTNCCGGCGGCAATTTGCTGCCGAATCGCACTTTCGAGAATGACNGCACCCCTGCGCCACCGANGAATCNAAAGTGAGG  
TTCTTGATCACGACCACCGGTTNGAGCCCTTGGGGCGTGAAGANCGCCTGCGCNATAACACCCGGGACGCTGCCACTC  
ATGTNCAGCGCTTCGCGANCTCNACATATCT

:::Rv81T7.seq:::

TCCTGGTGATCGANGGCCGCGGTTCCGGCCGAAAATCCGGTTCGGGTTCCGGGTCGCGGTTCCAACCTTGANCGGGTCC  
GCAGCTGATTCACCGTGGCAACGCCGGCCAACTGCGCATATGCGCATCCGAACCCTCACC GCCCGCCCGCGATCA  
CCCCAACCTGATCCAACGACAACCGCCCCCTCCCGCATACCCGGGCGCAGCGCGGAAACTCCGGCAACCGCGCGCCA  
CCGTGGCGATCGTGTGGGCGTTGCCTGACGAACANCCATCTTCCAGGCCACCAACCCCGCCACCGACCGCGCCCCG  
TCACACCCACAACCCGTGCGATCCAGCTCAGCCACGATCTCCACAATGCGCCCATCAATCGCATTGCGCTGAACGG  
GCAACTCCGCCAACTCCTCCAA

## Clone Rv82

:::Rv82SP6.seq:::

AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGATCTGGTACCCATCCGTGATA  
CATTGAGGCTGTTCCCTGGGGGTGCTTACCTTCCACGAGCAAAACACGTAGCCCTTCAGAGCCAGATCCTGAGCAAG  
ATGAACAGAACTGAGGTTTTGTAAACGCCACCTTTATGGGCGAGCAACCCCGATCACCAGGTGGAAATACGTCTTCAGC  
ACGTGCAATCGCGTACCAAACACATCAGCATATGATTAATTTGTTCAATTGTATAACCAACACGTTGCTCAACCCG





## Clone Rv8

:::Rv8SP6D.seq:::

TTAGGCGTGACGGCCACCGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTC  
GCCGACTTTCGCGGTTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGCG

:::Rv8T7D4.seq:::

CGTCACCCCGATGCGCCAGATCGGGGCTTCGCAGATAAAGCACGAACTGGCGGGCAAAACGTCGATCTCGGAGCCGG  
AAGGGCAATCAGCCGACCGTCGACGAACGACACCGGCGAGACCACTTAGGCAGTGACGGCCT

## Clone Rv90

:::Rv90SP6.seq:::

CTTTTCNCGATGTCTCATGATNCCNANGGAGAACNNTGCNANCNCNGCCGCTGACNTNGCNCACCGCTNTGGCNGNGG  
TGACATTGGTGGTGGTTGCGGGCTGCNACGCCCGACTCGANGCCGANCCATNTNTTGGCGCCGACCGCNTNTCGTCTC  
NACCGCANCCCCNATCTCNGCCGCNCCCGGTGGANCTACNGCTNCTTCGCCATCTCTCGCCNATGGCTCCNGCGNNTC  
GCNCAACGTNTGGTTTGGTNANCTGCCTACCTGGTCNT

:::Rv90T7.seq:::

GCTGCGCCAGTCGTTCCGGTGCGGTTCATGCCGTTGGACCNACCATCGGAGTTAGTTGCCGAACCGCGGACCACCGCAAG  
CACCCGGTCTTGGTTCGCGCACCGCGTCGGCCAACCGCTTGAGCACCACCACGCCGAGCCCTCGCCGCGCACGAATCC  
ATCCGCGTTGGCGTCNAANCTGTNGCATCGGTCGGTCGGTGACAGCGCCGACCACTTGGACAGCGCGATGGCGGTGAA  
CGGTNANTAGGTGACCTGCCNCCNCGCCGCCAATGCCACCTCCGCTTCACNCATGCGAATGGTCTGACACGCCNAG  
TGAATTGCCACCAGCGACAACAAAATCGGTATCTNCGCGACGGCGGACACGCNATCCCNACTGATACTCGATCCGC  
CCCACCGCTTGNANCTCCGGGTTCCNGTGCTCATGTACCNTCATGTCCGCTCTGCGCNCGATATTGACGATCGTGTTC  
CCACGANNANAGANCCTCATCACGCCGGTTTCGAGTGCCG

## Clone Rv91

:::Rv91SP6.seq:::

CTGTGTGCGGNCGGCGCGATATCGGCCCTTTTACTAACCGAACCCGATGTGGGCTCCGATCCGGCGCGCATGGCATCT  
ACNGCGACGCCGATCGATGACGGCCAGGCTTACGAGCTTGAGGGTGTGAANTTGTGGACCNCAACGGTGTGGTAGCG  
GACCTGCTANTGGTTATGGCGCGGGTACCGCGCAGTGAANGGCACCGAGGGGGAATCANCGCCTTTGTCGTCTANGCT  
GATTCCTCCCGGATCACCNCTGGAGCGCNCNCNANTTCATGGGACTGCGTGGCATCCAANACGGCGTGACCGGCTTCA  
TCCNTCNGGGTGCCCAAAGACAACCTTGATCNGCNGGAAGCGACGTCTGAANATCGCGCTGATCNACTCAACGCCGG  
ACGCTGTCTACCGGCGATCGCACCGGANTTGCCAANCCGCGCTNANNATNCGCNGAATGNCCGTCCACNANTGCAT  
GG

:::Rv91T7.seq:::

TGGGGTGCCGGGCGCCGAGTTGCGTCCCTGGGATCACGCAGAGTCGCCGGCGGGCTGCCGTTGGGCTATGAATTGCACC  
GAGCCGGAAAATCCGCANCAAACTGCGAGTAGCGGCCTGCAGAAGTGCANCTCGGCCGAAACGGAGTACGGTGGACA  
ACGAAAAGCGCCGCCGAACNACGCACTGGCCCCGAGGATTGGCGTCAATCGGCCCGCCCGTCCGAACTTGGGAAGANAC  
ANTGCGGTTCTACCGTGATCTGGTGGAATGCTCCAACNNACCTTCNCCGAAAGCTACGGAAGCNACGGCGCGCATNTT  
CGGCCTTCCCAGCTCGACCTGACGCTGGAAATCG

## Clone Rv92

:::Rv92SP6.seq:::

NGGCNNGGAAGTTAATGCCCTACTGGTTCNATGCTCNACNTCNCNGTGACNNCCTGCNCCGACCCGCCGAGGTCTCT  
GNCCGTNACCACCGANCGGCGATCCGGGACTCTNGTACGCATCCAACANNGANCAACGTGCACGGGCGGAGTNGTNC  
CGCCACTTCGNCNATGACGGGGTCGATCCNTTCGACGTCCGTGCGCGCGTCGGTCGAGTGGCGGTACNCTCCNNGTA  
CTCGACCNCACNGACGAGAGGACTCGANCCCATCTACGTGTGGACGAAACANATCTTCTGTCCNACGACTACACCACC  
ACCCAGGCCATCGCCGNCGCCGCGANGCCCTTCGACGCCNTACTGGTCCNNGNGGGCGCTCTCCGGTTGTCTNNC  
NCNTGNCGTGTTCTTCACNCACTGCCCNACATCGANCCCGAGCNATNCNANGTCCGTCAATC

:::Rv92T7.seq:::

GGACACTGTTGCGGTGCCCTCGTCAAAGCCGGAGTGGTGTGCTGCGCCGGACCCGACCCGACCTTCAGCGGGGGTT  
CACAGCTCCGTGGGTGCCGTTACTTCCGATCGCCGCGAGTGTGCGCGTGCCTGTGGCTGATGCTGAACCTCACCGCGTT  
GACTTGGATCCGTTTCGGGATCTGGCTGGTGCCGGAACCGGATTTATGTCNGCTACGGGCGCCGGCACTCGCGCA  
TGGCCTTCGGCAAGCNCNANANAACGCGACCCGGAGGTGTTGAACTAGCTTCGCCGCGTATTTACAAATTGCNTTATA  
TGTCTACACATAAGACGCAAACCTGCTCTATTGTCAANTCCCANCGTGGTGTGGCNCATGAAGATGTTTGG

## Clone Rv94

:::Rv94SP6.seq:::

TCCTTCTCGGTATCGGTTTGGGCTGTACCCANAGTTGGTAGTTCTTCACGTNCTGTTGTTTCGAGCGTCNAGCCGTCG  
CGCGTGTNANGTCNCCGGACGCGTATCCCGCCAGGCCGGTCANGGTGCCCTTCCANTCCACGCCGCTGTGGTCGGCG  
AACGCTNATCTTCAATCGAGACCATCGCCAGCTTCATCNTGTTGGCGATCTTGTTCNNACGGCACCTCNAACGGCGCT  
NCTAGTACNCCACNCNATCNTGTTNCCTTTCNCGTCNACATCCTCGATNCCNCNTGCACTTTCCTTCGANCNCTGGGC  
CGAGCCGTTGGCANTNACCTCNGAGCCCCATTGGACATCANCCANCCCGCCTGCGAACGGGAACGTCAGCNCNCTGG  
CGACAACCTGGCCAACAN

:::Rv94T7.seq:::

CACNCCGTGATCGNAGCCCCNGTAGAAATNGTTGAGCCAGTTGGTGCGGCGCTCGTTGCCGGCGGTNATCTCGTCGA  
GCTCNTCTTCCATCGCCGCGGTGAAGTCGTACTCGACNAGCCGACCNAATGCTGCTCNAGCAGACCGGTTACNNNA  
ACNCCNCCTCNTGACNGCACCAGTGCNCTGCCCTTCTTGTGCACGTACCCGCNATCCTGGATGGTCTTGATGATCNAC  
TANTNTGTCGACGGGCGGCCGATGCCCATCTCTCNAGCGCTTTGACCAGCGACNCTCGGTGTATCGGGCCGGCGGG  
TTNGTGCGATGGCCGTCTGGGGTCANCTCNACNATNTTCANCCGTTGACCCGGGGTCACA

## Clone Rv95

:::Rv95SP6.seq:::

TGGCCTTCTGNCANGGCGNNACATNNGCTATNGCGAGCGTGTAACCGATCATCNTCCNNGGCGACTGTGGCCTGANCG  
GCAAGGGTNGCCTNATTCNTCCTCCTGNGGCATGGTTNCCACACGGAATGNCGGTAAGTCTGGTCGGCAACCTGGCCC  
GCTGCGGGTTGGGTCGGATTGCTCGGCTANTAAGGTGCTCGCCTGGTGTNACNACTAATCNCNATATACNCTTANC  
GGGAGTNGNCGTCCCGATCTTNGCCCTGCCGCGGGCGATCNCGTTTCGCANACCCGCCACCGGAACCTCNCAANGTGCGC  
TCATCGGGCTCTACGCGCCATCTTCCCCGGATTCTTCGCGGCGNNGTNCNNGGGACCCCGGACTGTGACNGGCCCAA  
CGGCTCATCATCG

:::Rv95T7.seq:::

CCGGATAGCGGTGCTGAACTTCGCCCCTCCCTCCANCGATTGAGCTTCAGCCCGACCGGCAGGTNNGGAGTCGGC  
ATGCGGTCTTCGCCCCGACCCCGCTGGCTAAATANCCACCCCGAGCGCGGTACGGTCTTTGCACCGGGACGACGC  
ATACCGGCAGCGCGAACATCNCGCGGGCTGCGAGCNTGAACGTCCAATACCANTCNAACAGTGTCCGCGCGTNAAC  
CCGANCCGGCGGTGCTTCNGTAATCAACGGCTCCTGCGCAACCAGCTGCAAGTCGCCGGTGCCACCGGCGTTGACGA  
TCTTGATGTCTGCGANCTCGCGCACCAGCTCGACGGCCCCGGCA

## Clone Rv96

:::Rv96SP6.seq:::

CCTCCCGACCACATACAGGCAAAGTAATGGCATTACCGCGAGCCATTACTCCTACGCGCGCAATTAACGAATCCACCA  
TCGGGGCAGCTGGTGTGATAACGAAGTATCTTCAACCGGTTGAGTATTGAGCGTATGTTTTGGAATAACAGGCGCAC  
GCTTCATTATCTAATCTCCCAGCGTGGTTAATCAGACGATCGAAAATTTTCATTGCAGACAGGTTCCCAAATAGAAAG  
AGCATTTCTCCAGGCACAGTTGAAGAGCGTTGATCAATGGCCTGTTCAAAAACAGTTCTCATCCGGATCTGACCTTT  
ACCAACTTCATCCGTTTCACGTACAACATTTTTTAGAACCATGCTTCCCCAGGCATCCCGAATTTGCTCCTCCATCCA  
CGGGGACTGAGAGCCATTACTATTGCTGTATTTGGTAAGCAAAATACGT

## Clone Rv9

:::Rv9SP6.seq:::

CTTCACNTCCGTACGGCTCGGGTACGCTTCGGTCNCATTGTGCGAGTGATAGATGACGACCGGGACCTCGTCGGCATC  
TTCCATAGCCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGGTANAAGGTCGGCGANCGCTCNGCATTTGGTCAT  
CGGGATATGCCGCTCGGGACGGTCANAGCCTCGGGTCCGGCCAGCACTCCGCAAGGCTTCGTGGGGTGGTCGGGACG  
CGCATGGGCCACCATCGCATTCACAGGTCTGCGCGAATCACCAGCACGTANACGGTTCTTTCTAAGCAACACCGA  
ANTTTTCAGGACCCGAATGCTCCGGGAAACATGTACGGTAGGTGCGGTATTCCGGCTACCGGCTGANCATTTAGCACGC  
CGGCCAGCACCGCACGAACAGGCAATCAGCCGCCCGCCACCCGACCGCGG

:::Rv9T7.seq:::

CAGGCATGCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACCACGCGCGGGTCGGGCGCCGGGCC  
CGGGCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCACCCGGCTGCGCTACGTCGAGCCATACCGG  
GCGGAGCTACATCGGCTCGGCCGCCAGTGTTCCGGCCCTCTTCGAGGTGAGGTGATACCGATTGCGCATCCGC  
AGCCGCACCTGGACGACAGAACCGTGCCCTACGAATTGCTTGTGCGGGCGGGGCCAAAGAACAGCTTGGCATCCTGGC  
GCGATTGGCCGGCGCGGCGCTGGTCGCCAAGGAAGACCCGTTCCGGTGCTGAT

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**Table 4 :** End-sequences of the polynucleotide inserts cloned in the named recombinant BAC vectors contained in the I-2049 *M. bovis* strain Pasteur genomic DNA library.

RvXXXSP6 corresponds to the SP6 end-sequence of the clone RvXXX.

RvXXXT7 corresponds to the T7 end-sequence of the clone RvXXX.

RvXXXIS 1081 corresponds to a region located close to a copy of the IS1081 repetitive sequence (Insertion element).

The character « - » denotes an uncertain base residue.

#### Clone X0001

.....X0001SP6.seq:.....

AAG-

TCGGGTTTCCACACGCGCGGTTTGACCCTAGTCATATGTAATCATGTGTACCATGTGCGGGCGCTTTTCGACGGCCG  
CGAACCACCGGA-ATTTCTGTGATTTCACTGCGTACCATCTGGCACAATTGAGCA-TTGTCT-  
TCGCGGTGGTCGG-CGGGTTGCGTGCCGCTGCTGCGA-ATGCACCA-  
TAAGCCCGAACCACCGGCTTGGTGACCACCGCAGCTGCGTGTGGGGGTAACCACTCCGCGACCCCAAGGATGGT  
CATTTCCAATGAACCGGCTGGACTTCGTCCA-A

.....X0001T7.seq:.....

GTGCGGTTTCGATCGACCGGATCTTCACCTCGTAACCTCGATGCTTAGCAGGATCCAGCTTGACCGCGTTTGGCTCT  
ACCACTCTTTGAGTGGCGCCGTCGCTGTGCCCCATCGGTGTTTCATGACGAACGCTTCGAAAGACTTCCTCTTGTG  
AGCCGGAATGTCTGCGTAAAGAAGTTCCATGTCCGGGAAGTAGACCCGGTCGCCCTCCACGTGGTACTCCTTCGAGG  
TCCGCTTCTCGCCGGATCCGATAAACACCGGCCCCAGGCACCGCAGCGTGAGTTCGAACGGCTTCAGGTAGGTGTTT  
ATGCGGCGGACTCCGGGAGTGCGAGAAATAGCGGTGCGCGGTAGCTGTAGACCGGATGGTTTCCGCCAGGCTGACG  
TCGAAGATGCCTCCTTGAAGGGGCGCGA

#### Clone X0002

.....X0002SP6.seq:.....

AACTCAAGTTTTTACGGTGATCGCGCATCACCTGGTTCATGAAGTGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCA  
ACATGAGCCAGCCTCTCGTCGGCGGTGGGTGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCTGAAA  
CCAGCTTCCATATCCCGCGAC-  
AACGACGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCGTTCCTCCACCGACCGGGCCCGG  
TGT

.....X0002T7.seq:.....

GTGCAGGTTTCGACAATGTGGTGCCGGTTTCGGCGGCTACGTGCCATCGAGACACTGGCGCA-GCTATCGCACCCGTT  
ATCGGCTGCGAGCAAATCGCGGTATGCGTTCTTGAGCATGAGTCGGCGACCGTCGTCATGGTCGACACCCACGACGG  
AAAGACGCAGATCGCCGTCAAGCATGTGTGCCGCGGATTATCAGGACTGACCTCCTGGCTGACCGGCATGTTTGGTC  
GCGATGCCTGGCGCCCGGCCGCGTGGTTCGTGGTTCGGCTCGGATAGCGAGGTGAGCGAATTCGTGGCAGCTCGAA  
AGGGTCCTGCCGGTGCCGGT

#### Clone X0003

.....X0003SP6.seq:.....

TTCGAGTCATGCGCCCGCTCGACACGAA-ATGCACGTCG-  
GGTTCGATCGACCCGATCTTCACCTCGTAACCTCGATGCTTAGCAGGATCCAGCTTGACCGCGTTTGGCTCTACCCA  
CTCTTTGAGTGGCGCGTGCCTGTGCCCCATCGGTGTTTCATGACGAACGCTTCGAAAGACTTCCTCTTGTGAGCCG  
GAATGCTGCGTAAAGAAGTTCCATGTCCGGGAAGTAGACCCGGTCGCCCTCCACGTGGTACTCCTTCGAGGTCCGC  
TTCTC



.....X0009T7.seq:.....  
CGCCCAGGGCCGCTCCCGGGCGACCCGACCATTTGCTGTGCGCCGCGTAACGCCATCACGGATGACGCGCAGTTTCGTCTG  
CTGTCTAGTCTCCACCATCGCTGCACACCGGGCGGCCAGGACCCATTGGCCGTGCGACTCGTAGAGCAGGTAATCCTC  
GTCGACGGACTCGGTAACCAACCGCCGCCAGCTCCGCTGCCAGGTGCGCGGGGTTGACACCGGCGGGCATCGGGATGG  
ACGACGACGCGGTGCTGACGGCGCCTGTCGCGACGCTGAGCTCGGACACAGCTAGTAAATGTAGCCTAACCTACTTA  
ATGGGTCGACGCCCCCGGGGTGCTGCGATGTCCAACGTTGCTCGACTGGAAGAAAATGCTCGTGGGGAGCAAATG  
GCACC

## Clone X0010

.....X0010SP6.seq:.....  
AATACTCAATCTTGATCGGTTTCAGCAACAGCCGATCGACGGCTTCGCCCAGGGCCGCTCCCGGGCGACCCGACCA  
TTGCTGTGCGCCGCTAACGCCATCACGGATGACGCGCAGTTTCGTGCTGTCTAGCTCCACCATCGCTGCACACCGG  
CGGCCAGGACCCATTGGCCGTCGCACTCGTAGAGCAGGTAATCCTCGTGCACGGACTCGGTAACCAACCGCCGCCAGC  
TCCGCTGCCAGGTCGGCGGGGTTGACACCGGCGGGCATCGGGATGGACGACGACGCGGTGCTGACGGCGCCTGTCGC  
GACTCTGAGCTCGG

.....X0010T7.seq:.....  
GGATGTGCTGTGAGCGCCGACCAACAGCGCCGACGCTAAGGATGGAACGCACGGCATCTTCTGACGCGTAACCGCG  
TTGTGATCGCGAGCTGAGGAGACGGTATGGGGGAGGGTTCTCGGAGGCCATCTGGGATGTTGATGTCTGTCGATCTT  
GAGCCGGTGCAACTCGTCGGCCCGGACGGTACGCCGACGGCCGAACGCCGCTACCACCGTGACCTTCCTGAGGAAAC  
GCTGCGTTGGCTCTACGAGATGATGGTGGTCACCCGCGAGCTGGATAACGAATTCGTCAATCTGCAGCGCCAGGGGG  
AAGCTGGCGTTGTACACGCCCTGTCGCGGGCAGGAAGCCGCGCAGGTGGGTGCGGCGGCTTGCCTACGCAAAACCGA  
CTGGTTGTTCCCC

## Clone X0012

.....X0012SP6.seq:.....  
ATCACGACAACAGCGACGGTGTGTCGGATCAGCGGCCCCCGTTGCCGGGCAATGTTGAGGCGTTTCTGCGTCTGGTT  
GAGGCCGGCTGGGAC-  
CCGAGGTGGTCTCGGCCACATGGGCAGCACACCACCGTGGTGATGCATCTAGACGTGCAGGACCGTGCCGCTGGC  
CTGCA

.....X0012T7.seq:.....  
GCGGCTACGTGCCATCGAGACACTGGCGCAGGCTATCGCACCCGTTATCGGCTGCGAGCAAATCGCGGTATGCGTTC  
TTGAGCATGAGTCGGCGACCGTCGTCTATGGTTCGACACCCACGACGGAAAGACGCAGATCGCCGTCAAGCATGTGTGC  
CGCGGATTATCAGGACTGACCTCCTGGCTGACCGGCATGTTTGGTTCGCGATGCCTG:

## Clone X00013

.....X0013T7.seq:.....  
TACAAGCGGCACCTCGCCGGTGAACCTGACCGTTGCGACGCTGCGCACCGCCGCCGGGCGCGTGCTCGGCGCGCCGGC  
GGCCCCGAGGCTGAGAGGGGAACCAACCATGCAGGTGAACATGACGGTAAACGGCGAGCCCGTCACCGCCGAGGT  
CGAACCCCGGATGCTGCTGGTCCATTTTCTCCGTGATCAGCTGCGGCTCACCGGAACCTCACTGGGGCTGTGATACCA  
GCAACTGCGGGACATGCGTGGTGAGGTCGACGGCGTGCCGGTGAAATCCTGCACGATGCTCGCCGTGATGGCTCC  
GGG

## Clone X0014

.....X0014T7.seq:.....  
AGCGGCTGGTTACGACTCCCTGTTTGTGATGGACCACTTCTACCAACTGCCCATGTTGGGGACGCCCG-CC-  
TCCGATGCTGGAAGCCTACACTGCCCTTGGTGCGCTGGCC-C-GCGACCGAGCGGCTGCAACTGGGCGC-  
TTGGTGACC-GCAATACCTACCGCACCCC-ACCCTGCTGG-CAAA-  
ATCATACCACGCTCGACTTGGTTAGCGCCGGTCGA-CGATCCTCGGCATTGGAACCGGTTGGTTT-

## Clone X0015

.....X0015SP6.seq:.....  
ACGCGCGCCGATCATATCTGCTATGGATGTACAATTGAGTCTTGTGCTGTTATACCAGTATATGGTGTACTATTTGAT  
CTATGCTGACGTGTGAGATGCGGGAATCGGCCCTGGCTCGACTCGGCCGGGCTCTGGCTGATCCGACGCGGTGCCGG  
ATTCTGGTGGCGTTGCTGGATGGCGTTTGTATCCCGGCCAGCTAGCTGCGCACCTCGGGTTGACCCGATCGAATGT  
GTCCAACCATCTGCTGTTTGGCGGGGCTGCGGGCTGGTA-TCCCAACCTATGAGGGCCGGCAGGTTTCGGTAT













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CLAIMS

1. A method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone belonging to a genomic DNA library of a given mycobacterium strain, said DNA library being cloned in a bacterial artificial chromosome (BAC) vector.
2. The method according to claim 1, wherein the BAC-based DNA library has been constructed from genomic DNA of *Mycobacterium tuberculosis*.
3. The method according to claim 2, wherein the BAC-based DNA library has been constructed from genomic DNA of *Mycobacterium tuberculosis* strain H37Rv.
4. The method according to claim 3, wherein the BAC-based DNA library has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on November 19, 1997 under the accession number I-1945.
5. The method according to claim 1, wherein the BAC-based DNA library has been constructed from genomic DNA of *Mycobacterium bovis*.
6. The method according to claim 5, wherein the BAC-based DNA library has been constructed from the genomic DNA of *Mycobacterium bovis* BCG strain Pasteur.
7. The method according to claim 6, wherein said DNA library contains approximatively 1600 clones and wherein the genomic DNA is cloned into a recombinant pBeloBAC11 vector with an average insert size of approximately 80 kb.
8. The method according to claim 6 or 7, wherein the at least one BAC-based DNA library has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on June 30, 1998 under the accession number I-2049.

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9. A method of isolating a polynucleotide of interest that is present in a genome of a first mycobacterium strain or that is expressed by the first mycobacterium strain and that is absent or altered in a genome of a second mycobacterium strain or that is not expressed by the second mycobacterium strain, said method comprising :

- a) providing at least one polynucleotide contained in a clone of a bacterial artificial chromosome (BAC) DNA library of the first mycobacterium strain;
- b) providing at least one genomic or cDNA polynucleotide from a second mycobacterium strain that is different from the first mycobacterium strain or at least one polynucleotide contained in a clone of a BAC DNA library prepared from the genome of the second mycobacterium strain;
- c) contacting under hybridizing conditions the polynucleotide of step a) with the polynucleotide of step b); and
- d) isolating the polynucleotide of step a) that has not formed a hybrid complex with the polynucleotide of step b).

10. The method of claim 9, wherein the polynucleotide contained in a clone of a BAC DNA library of the first or second mycobacterium strain is prepared by the following procedure :

- 1) digesting at least one recombinant BAC clone by an appropriate restriction endonuclease to yield a polynucleotide insert of interest; and
- 2) isolating the polynucleotide insert of interest.

11. A purified polynucleotide of interest that has been isolated according to the method of claim 9.

12. The purified polynucleotide of claim 11 which contains at least one Open Reading Frame (ORF).

13. The purified polynucleotide of claim 12, which is SEQ ID N0:1.

14. The purified polynucleotide of claim 12, wherein said polynucleotide is selected from the group consisting of :

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- a) a polynucleotide comprising at least 8 consecutive nucleotides of SEQ ID N0:1;
- b) a polynucleotide having a sequence fully complementary to SEQ ID N0:1; and
- c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).
- 15 15. The purified polynucleotide of claim 14, which is SEQ ID N0:2.
16. The purified polynucleotide of claim 14, which is SEQ ID N0:3.
17. The purified polynucleotide of claim 12, wherein the ORF encodes all or part of a polypeptide involved in the pathogenicity of a mycobacterium strain.
- 10 18. The purified polynucleotide of claim 12, wherein the ORF encodes all or part of a Polymorphism Glycine Rich Sequence (PGRS).
19. The purified polynucleotide of claim 18, which is SEQ ID N0:4.
20. The purified polynucleotide of claim 18, which is selected from the group consisting of:
- 15 a) a polynucleotide comprising at least 8 consecutive nucleotides the of SEQ ID N0:5 ;
- b) a polynucleotide having a sequence that is fully complementary to SEQ ID N0:5 ;
- c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).
- 20 21. A pair of the purified polynucleotides as claimed in claim 11.
22. A *Mycobacterium tuberculosis* strain Rv37 genomic DNA library that has been deposited in the Collection Nationale de Cultures de Microorganismes under accession number I-1945, wherein said genomic DNA library comprises
- 25 recombinant bacterial artificial chromosome vectors.
23. A recombinant bacterial artificial chromosome (BAC) vector, which belongs to the genomic DNA library of claim 22.
24. The recombinant BAC vector of claim 23, which is selected from the group consisting of :

11 21 08 00

- Rv101; Rv102; Rv103; Rv104; Rv105; Rv106; Rv107; Rv108; Rv109; Rv10;
- Rv110; Rv111; Rv112; Rv113; Rv114; Rv115; Rv116; Rv117; Rv118; Rv119;
- Rv11; Rv120; Rv121; Rv122; Rv123; Rv124; Rv126; Rv127; Rv128; Rv129;
- Rv130; Rv132; Rv134; Rv135; Rv136; Rv137; Rv138; Rv139; Rv13; Rv140;
- 5 Rv141; Rv142; Rv143; Rv144; Rv145; Rv146; Rv147; Rv148; Rv149; Rv14;
- Rv150; Rv151; Rv152; Rv153; Rv154; Rv155; Rv156; Rv157; Rv159; Rv15;
- Rv160; Rv161; Rv162; Rv163; Rv164; Rv165; Rv166; Rv167; Rv169; Rv16;
- Rv170; Rv171; Rv172; Rv173; Rv174; Rv175; Rv176; Rv177; Rv178; Rv179;
- Rv17; Rv180; Rv181; Rv182; Rv183; Rv184; Rv185; Rv186; Rv187; Rv188;
- 10 Rv18; Rv190; Rv191; Rv192; Rv193; Rv194; Rv195; Rv196; Rv19; Rv1; Rv201;
- Rv204; Rv205; Rv207; Rv209; Rv20; Rv214; Rv215; Rv217; Rv218; Rv219;
- Rv21; Rv220; Rv221; Rv222; Rv223; Rv224; Rv225; Rv226; Rv227; Rv228;
- Rv229; Rv22; Rv230; Rv231; Rv232; Rv233; Rv234; Rv235; Rv237; Rv240;
- Rv241; Rv243; Rv244; Rv245; Rv246; Rv247; Rv249; Rv24; Rv251; Rv252;
- 15 Rv253; Rv254; Rv255; Rv257; Rv258; Rv259; Rv25; Rv260; Rv261; Rv262;
- Rv263; Rv264; Rv265; Rv266; Rv267; Rv268; Rv269; Rv26; Rv270; Rv271;
- Rv272; Rv273; Rv274; Rv275; Rv276; Rv277; Rv278; Rv279; Rv27; Rv280;
- Rv281; Rv282; Rv283; Rv284; Rv285; Rv286; Rv287; Rv288; Rv289; Rv28;
- Rv290; Rv291; Rv292; Rv293; Rv294; Rv295; Rv296; Rv29; Rv2; Rv301;
- 20 Rv302; Rv303; Rv304; Rv306; Rv307; Rv308; Rv309; Rv30; Rv310; Rv311;
- Rv312; Rv313; Rv314; Rv315; Rv316; Rv317; Rv318; Rv319; Rv31; Rv32;
- Rv322; Rv327; Rv328; Rv329; Rv32; Rv330; Rv331; Rv333; Rv334; Rv335;
- Rv336; Rv337; Rv338; Rv339; Rv33; Rv340; Rv341; Rv343; Rv344; Rv346;
- Rv347; Rv348; Rv349; Rv34; Rv350; Rv351; Rv352; Rv353; Rv354; Rv355;
- 25 Rv356; Rv357; Rv358; Rv359; Rv35; Rv360; Rv361; Rv363; Rv364; Rv365;
- Rv366; Rv367; Rv368; Rv369; Rv36; Rv370; Rv371; Rv373; Rv374; Rv375;
- Rv376; Rv377; Rv378; Rv379; Rv37; Rv381; Rv382; Rv383; Rv384; Rv385;
- Rv386; Rv387; Rv388; Rv389; Rv38; Rv390; Rv391; Rv392; Rv393; Rv396;
- Rv39; Rv3; Rv40; Rv412; Rv413; Rv414; Rv415; Rv416; Rv417; Rv418; Rv419;

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Rv41; Rv42; Rv43; Rv44; Rv45; Rv46; Rv47; Rv48; Rv49; Rv4; Rv50; Rv51;  
Rv52; Rv53; Rv54; Rv55; Rv56; Rv57; Rv58; Rv59; Rv5; Rv60; Rv61; Rv62;  
Rv63; Rv64; Rv65; Rv66; Rv67; Rv68; Rv69; Rv6; Rv70; Rv71; Rv72; Rv73;  
Rv74; Rv75; Rv76; Rv77; Rv78; Rv79; Rv7; Rv80; Rv81; Rv82; Rv83; Rv84;  
5 Rv85; Rv86; Rv87; Rv88; Rv89; Rv8; Rv90; Rv91; Rv92; Rv94; Rv95; Rv96  
and Rv9.

25. The recombinant BAC vector of claim 23, which is selected from the group consisting of:

Rv234; Rv351; Rv166; Rv35; Rv415; Rv404; Rv209; Rv272; Rv30; Rv228;  
10 Rv233; Rb38; Rv280; Rv177; Rv48; Rv374; Rv151; Rv238; Rv156; Rv92; Rv3;  
Rv403; Rv322; Rv243; Rv330; Rv285; Rv233; Rv219; Rv416; Rv67; Rv222;  
Rv149; Rv279; Rv87; Rv273; Rv266; Rv25; Rv136; Rv414; Rv13; Rv289; Rv60;  
Rv104; Rv5; Rv165; Rv215; Rv329; Rv240; Rv19; Rv74; Rv411; Rv167; Rv56;  
Rv80; Rv164; Rv59; Rv313; Rv265; Rv308; Rv220; Rv258; Rv339; Rv121;  
15 Rv419; Rv418; Rv45; Rv217; Rv134; Rv17; Rv103; Rv21; Rv22; Rv2; Rv270;  
Rv267; Rv174; Rv257; Rv44; Rv71; Rv7; Rv27; Rv191; Rv230; Rv128; Rv407;  
Rv106; Rv39; Rv255; Rv74; Rv355; Rv268; Rv58; Rv173; Rv264; Rv417;  
Rv401; Rv144; Rv302; Rv81; Rv163; Rv281; Rv221; Rv420; Rv175; Rv86;  
Rv412; Rv73; Rv269; Rv214; Rv287; Rv42 and Rv143.

20 26. A *Mycobacterium bovis* BCG strain Pasteur genomic DNA library, wherein said genomic DNA library comprises recombinant bacterial artificial chromosome vectors.

27. A *Mycobacterium bovis* BCG strain Pasteur genomic DNA library according to claim 26, wherein said DNA library contains approximatively 1600  
25 clones and wherein the genomic DNA is cloned into a recombinant pBeloBAC11 vector with an average insert size of approximately 80 kb.

28. A *Mycobacterium bovis* BCG strain Pasteur genomic DNA library according to claim 26, that has been deposited in the Collection Nationale de

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Cultures de Microorganismes (CNCM) on June 30, 1998 under the accession number I-2049.

29. A recombinant bacterial artificial chromosome (BAC) vector, which belongs to the genomic DNA library of claims 26 to 28.

5        30. A recombinant BAC vector according to claim 29, which is selected from the group consisting of:

X0001; X0002; X0003; X0004; X0006; X0007; X0008; X0009; X0010; X0012; X0013; X0014; X0015; X0016; X0017; X0018; X0019; X0020; X0021 and X0175.

10        31. A method for detecting a mycobacterial nucleic acid in a biological sample comprising the steps of:

- a) contacting the recombinant BAC vector according to claim 23 or 29, or a purified polynucleotide according to claim 11 with the mycobacterial nucleic acid in the biological sample ; and
- 15        b) detecting a hybrid nucleic acid molecule formed between said recombinant BAC vector or said purified polynucleotide and the mycobacterial nucleic acid in the biological sample.

20        32. The method of claim 31, further comprising before step a), making the mycobacterial nucleic acid in the biological sample available to a hybridization reaction.

33. A method for detecting mycobacterial nucleic acid in a biological sample comprising the steps of:

- a) contacting a first polynucleotide according to claim 11 that has been immobilized onto a substrate with the mycobacterial nucleic acid in the biological sample ; and
- 25        b) contacting a hybrid nucleic acid molecule formed between said first polynucleotide and the mycobacterial nucleic acid in the biological sample with a second, labeled polynucleotide according to claim 11, wherein said

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second polynucleotide and said first polynucleotide have non-overlapping sequences.

34. The method of claim 33, further comprising before step a), making the mycobacterial nucleic acid in the biological sample available to a hybridization  
5 reaction.

35. The method of claim 33 or 34, further comprising before step b), removing the mycobacterial nucleic acid that is not hybridized with the immobilized first polynucleotide.

36. A method for detecting mycobacterial nucleic acid in a biological  
10 sample comprising the steps of:

- a) contacting the mycobacterial nucleic acid in the biological sample with a pair of purified polynucleotides according to claim 21 ;
- b) amplifying said mycobacterial nucleic acid ; and
- c) detecting the amplified mycobacterial nucleic acid.

37. The method of claim 36, further comprising before step a), making the mycobacterial nucleic acid in the biological sample available to a hybridization  
15 reaction.

38. A kit for detecting a mycobacterium in a biological sample comprising:

- a) a recombinant BAC vector according to claim 23 or 29, or a purified  
20 polynucleotide according to claim 11 ; and
- b) reagents necessary to perform a nucleic acid hybridization reaction.

39. A kit for detecting a mycobacterium in a biological sample comprising:

- a) a recombinant BAC vector according to claim 23 or 29, or a first polynucleotide according to claim 11 that is immobilized onto a substrate ;
- 25 b) reagents necessary to perform a nucleic acid hybridization reaction ; and
- c) a second polynucleotide according to claim 11, wherein said second polynucleotide is radioactively or non-radioactively labeled, and wherein said second polynucleotide and said first polynucleotide have non-overlapping sequences.

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40. A kit for detecting a mycobacterium in a biological sample comprising:

- a) a pair of purified polynucleotides according to claim 20 ; and
- b) reagents necessary to perform a nucleic acid amplification reaction.

41. A method for detecting the presence of a genomic DNA, a cDNA or a mRNA of a mycobacterium in a biological sample, comprising the steps of:

- a) contacting the biological sample with a plurality of BAC vectors according to claim 23 or 29, or purified polynucleotides according to claim 11 that are immobilized on a substrate ; and
- b) detecting the hybrid complexes formed.

42. A kit for detecting a genomic DNA, a cDNA or a mRNA of a mycobacterium in a biological sample, comprising:

- a) a substrate on which a plurality of BAC vectors according to claim 23 or 29, or purified polynucleotides according to claim 11 have been immobilized.

43. A method for detecting a polynucleotide of mycobacterial origin in a biological sample, said method comprising:

- a) aligning at least one polynucleotide contained in a recombinant BAC vector according to claim 23 or 29 on the surface of a substrate ;
- b) contacting the polynucleotide in the biological sample with the substrate on which the polynucleotide of step a) has been aligned ; and
- c) detecting a hybrid nucleic acid molecule formed between the polynucleotide in the biological sample and the aligned polynucleotide of step a).

44. A kit for detecting a polynucleotide of mycobacterial origin in a biological sample, comprising:

- a) a substrate on which at least one polynucleotide contained in a recombinant BAC vector according to claim 23 or 29 has been aligned.

45. The method of claim 10, wherein the procedure by which the polynucleotide contained in a clone of a BAC DNA library is prepared, further comprises amplifying the polynucleotide insert.

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46. The method of claim 10, wherein the procedure by which the polynucleotide contained in a clone of a BAC DNA library is prepared, further comprises digesting the polynucleotide insert with at least one restriction endonuclease.

5 47. The method of claim 45, further comprising digesting the amplified polynucleotide insert with at least one restriction endonuclease.

48. The Polynucleotide of claim 17, wherein the mycobacterium strain is *Mycobacterium tuberculosis*.

49. The method of claim 36, wherein the amplified mycobacterial DNA is  
10 detected by gel electrophoresis or with a labeled polynucleotide according to claim 11.

50. The kit of claim 40, further comprising a polynucleotide according to claim 11.

51. The kit of claim 42, further comprising reagents necessary to perform a  
15 hybridization reaction.

52. A method for physically mapping a polynucleotide of mycobacterial origin in a biological sample, said method comprising:

- a) aligning at least one polynucleotide contained in a recombinant BAC vector according to claim 23 or 29 on the surface of a substrate;
- 20 b) contacting the polynucleotide in the biological sample with the substrate on which the polynucleotide of step a) has been aligned under hybridizing conditions; and
- c) detecting the location of the hybridized polynucleotide from the biological sample.

25 53. The kit of claim 44, further comprising reagents necessary for labeling DNA and reagents necessary for performing a hybridization reaction.

A

P O O L S

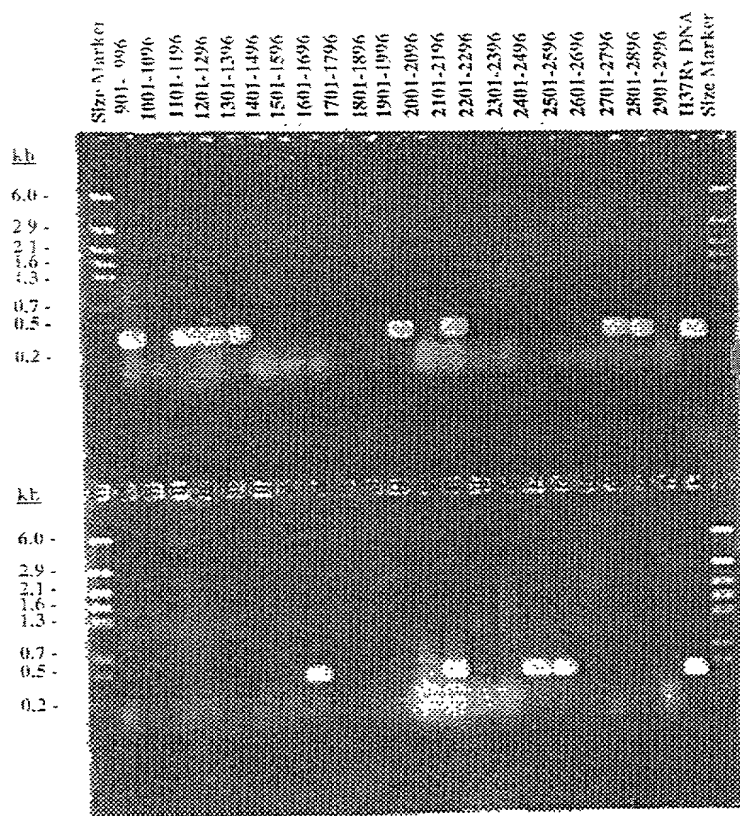


FIGURE 1A

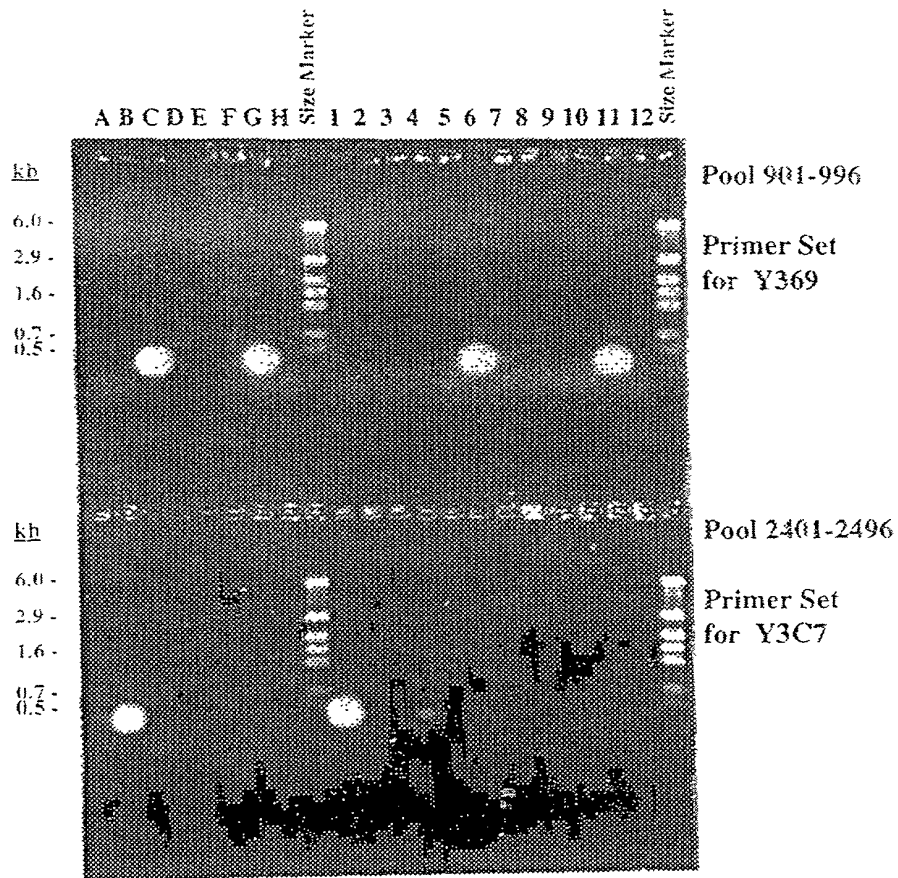
**B**

FIGURE 1B





A

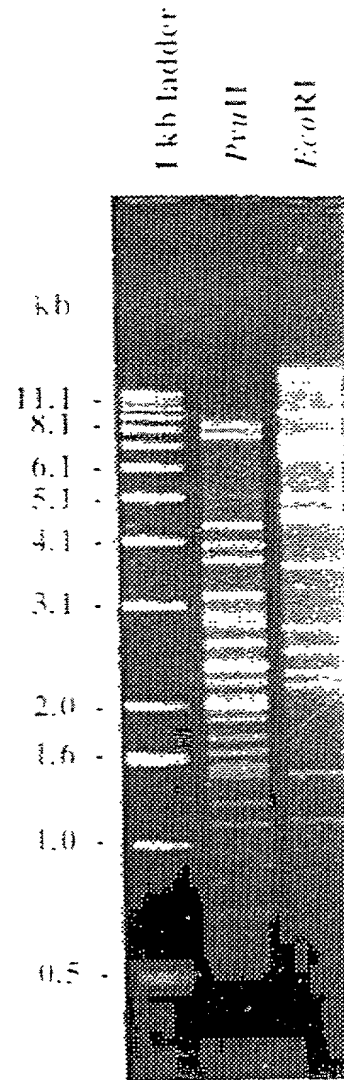


FIGURE 4A

B

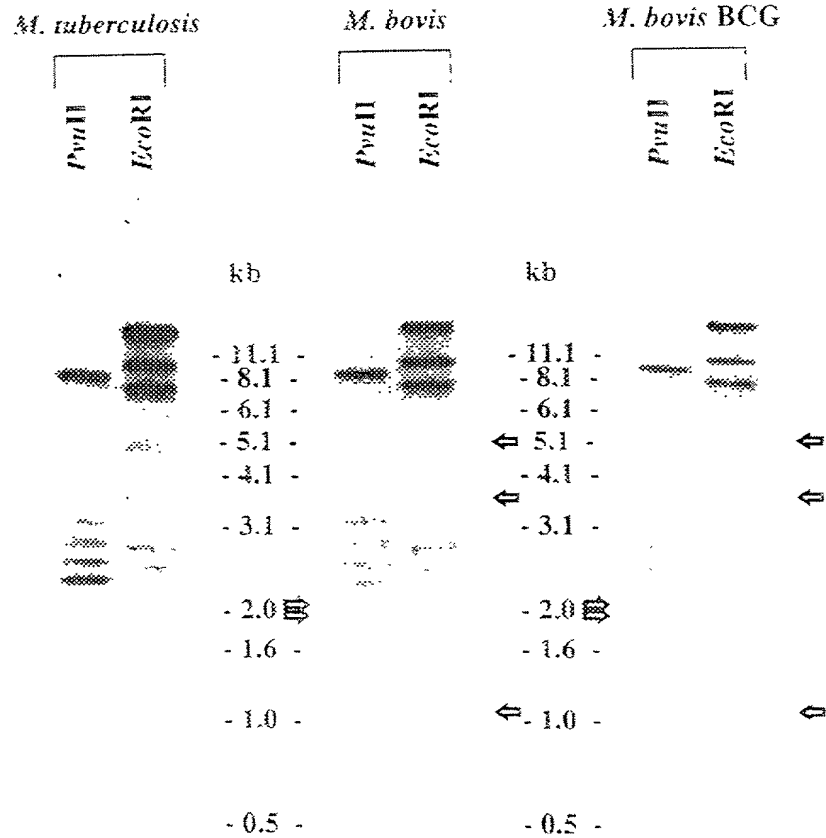


FIGURE 4B





pBeloBAC11

GCGGGCGGAA GGGGTTTCGCG TCAGCGGGTG TTGGCGGGTG TCGGGGCTGG

*NotI* restriction site

CTTAACTATG CGGCATCAGA GCAGATTGTA CTGAGAGTGC ACCATATGCG

GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC ATCAGGCGCC

ATTCGCCATT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC

TCTTCGCTAT TACGCCAGCT GGCGAAAGGG GGATGTGCTG CAAGGCGATT

primer T7-BAC1

AAGTTGGGTA ACGCCAGGGT TTTCCCAGTC ACGACGTTGT AAAACGACGG

CCAGTGAAT TGTAATACGAC TCAGTATAGG GCGAATTCGA GCTCGGTACC

T7-promoter sequence

CGGGGAT TCCTCTAGAGTCGA CCTGCAGGCA TGC AAGCTTG AGTATTCGAT

primer T7-Belo2

*HindIII* cloning site

SP6-promoter

AGTGTACCTTAAATAGCTTG GCGTAATCATGGTCATAGCTGTTT CCTGTG

sequence (complementary strand)

primer SP6-Mid (complementary strand)

TGAAATTGTT ATCCGCTCAC AATTCACAC AACATACGAG CCGGAAGCAT

AAAGTGTAAG GCCTGGGCT TG CCAATGAGT GAGCTAAC ACATTAATTG

primer SP6-BAC1 (complementary strand)

CGTTGCGCTC ACTGCCCCTG TTCCAGTCGG GAAACCTGTC GTGCCAGCTG

CATTAATGAA TCGGCCAACG CGAACCCTT GCGGGCGG CC GGGCCGTCGA

*NotI* restriction site

FIGURE 7

## DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that: my residence, post office address and citizenship are as stated below next to my name; I believe I am the original, first, and sole inventor (if only one name is listed below) or an original, first, and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled: **A method for isolating a polynucleotide of interest from the genome of a mycobacterium using a BAC-based DNA library. Application to the detection of mycobacteria** the specification of which ☐ is attached and/or ☒ was filed on **April 16, 1999** as United States Application Serial No. \_\_\_\_\_ or PCT International Application No. **PCT/IB99/00740** and was amended on \_\_\_\_\_ (if applicable)

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above. I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR § 1.56.

I hereby claim foreign priority benefits under 35 U.S.C. § 119(a)-(d) or § 365(b) of any foreign application(s) for patent or inventor's certificate or § 365(a) of any PCT international application(s) designating at least one country other than the United States, listed below and have also identified below, any foreign application(s) for patent or inventor's certificate, or any PCT International application(s) having a filing date before that of the application(s) of which priority is claimed:

Country	Application Number	Date of Filing	Priority Claimed Under 35 U.S.C. 119
<b>US</b>	<b>09/060 756</b>	<b>16/04/1998</b>	<input type="checkbox"/> YES <input type="checkbox"/> NO
			<input type="checkbox"/> YES <input type="checkbox"/> NO

I hereby claim the benefit under 35 U.S.C. § 119(e) of any United States provisional application(s) listed below:

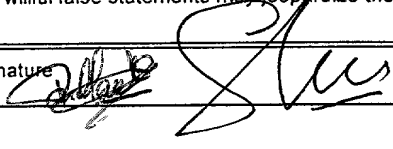
Application Number	Date of Filing

I hereby claim the benefit under 35 U.S.C. § 120 of any United States application(s) or § 365(c) of any PCT International application(s) designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application(s) in the manner provided by the first paragraph of 35 U.S.C. § 112, I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR § 1.56 which became available between the filing date of the prior application(s) and the national or PCT International filing date of this application.

Application Number	Date of Filing	Status (Patented, Pending, Abandoned)

I hereby appoint the following attorney and/or agent(s) to prosecute this application and transact all business in the Patent and Trademark Office connected therewith: **FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, L.L.P.**, Douglas B. Henderson, Reg. No. 20,291; Ford F. Farabow, Jr., Reg. No. 20,630; Arthur S. Garrett, Reg. No. 20,338; Donald R. Dunner, Reg. No. 19,073; Brian G. Brunsvold, Reg. No. 22,593; Tipton D. Jennings, IV, Reg. No. 20,645; Jerry D. Voight, Reg. No. 23,020; Laurence R. Hefter, Reg. No. 20,827; Kenneth E. Payne, Reg. No. 23,098; Herbert H. Mintz, Reg. No. 26,694; C. Larry O'Rourke, Reg. No. 26,014; Albert J. Santorelli, Reg. No. 22,610; Michael C. Elmer, Reg. No. 25,857; Richard H. Smith, Reg. No. 20,609; Stephen L. Peterson, Reg. No. 26,326; John M. Romary, Reg. No. 26,331; Bruce C. Zotter, Reg. No. 27,680; Dennis P. O'Reilly, Reg. No. 27,932; Allen M. Sokal, Reg. No. 26,695; Robert D. Bajefsky, Reg. No. 25,387; Richard L. Stroup, Reg. No. 28,478; David W. Hill, Reg. No. 28,220; Thomas L. Irving, Reg. No. 28,619; Charles E. Lipsey, Reg. No. 28,165; Thomas W. Winland, Reg. No. 27,605; Basil J. Lewis, Reg. No. 28,818; Martin I. Fuchs, Reg. No. 28,508; E. Robert Yoches, Reg. No. 30,120; Barry W. Graham, Reg. No. 29,924; Susan Haberman Griffen, Reg. No. 30,907; Richard B. Racine, Reg. No. 30,415; Thomas H. Jenkins, Reg. No. 30,857; Robert E. Converse, Jr., Reg. No. 27,432; Clair X. Mullen, Jr., Reg. No. 20,348; Christopher P. Foley, Reg. No. 31,354; John C. Paul, Reg. No. 30,413; Roger D. Taylor, Reg. No. 28,992; David M. Kelly, Reg. No. 30,953; Kenneth J. Meyers, Reg. No. 25,146; Carol P. Einaudi, Reg. No. 32,220; Walter Y. Boyd, Jr., Reg. No. 31,738; Steven M. Anzalone, Reg. No. 32,095; Jean B. Fordis, Reg. No. 32,984; Barbara C. McCurdy, Reg. No. 32,120; James K. Hammond, Reg. No. 31,964; Richard V. Burgujian, Reg. No. 31,744; J. Michael Jakes, Reg. No. 32,824; Dirk D. Thomas, Reg. No. 32,600; Thomas W. Banks, Reg. No. 32,719; Christopher P. Isaac, Reg. No. 32,616; Bryan C. Diner, Reg. No. 32,409; M. Paul Barker, Reg. No. 32,013; Andrew Chanho Sonu, Reg. No. 33,457; David S. Forman, Reg. No. 33,694; Vincent P. Kovalick, Reg. No. 32,867; James W. Edmondson, Reg. No. 33,871; Michael R. McGurk, Reg. No. 32,045; Joann M. Neth, Reg. No. 36,363; Gerson S. Panitch, Reg. No. 33,754; Cheri M. Taylor, Reg. No. 33,216; Charles E. Van Horn, Reg. No. 40,266; and Linda A. Wadler, Reg. No. 33,218; and \_\_\_\_\_. Please address all correspondence to **FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, L.L.P.** 1300 I Street, N.W., Washington, D.C. 20005, Telephone No. (202) 408-4000.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Full Name of First Inventor <b>1-00 COLE Stewart</b>	Inventor's Signature 	Date <b>Nov. 3, 2000</b>
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Listing of Inventors Continued on Page 2 hereof. ☐ Yes ☐ No

Listing of Inventors Continued From Page 1 hereof.

Full Name of Second Inventor <u>2-00</u> <u>BUCHRIESER-BROSCH Roland</u>	Inventor's Signature <u>[Signature]</u>	Date <b>Nov. 3, 2000</b>
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Residence <u>77680 ROISSY EN BRIE, FRANCE</u>		Citizenship <u>FR</u>
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Residence		Citizenship
Post Office Address		
Full Name of Sixth Inventor	Inventor's Signature	Date
Residence		Citizenship
Post Office Address		
Full Name of Seventh Inventor	Inventor's Signature	Date
Residence		Citizenship
Post Office Address		
Full Name of Eighth Inventor	Inventor's Signature	Date
Residence		Citizenship
Post Office Address		
Full Name of Ninth Inventor	Inventor's Signature	Date
Residence		Citizenship
Post Office Address		
Full Name of Tenth Inventor	Inventor's Signature	Date
Residence		Citizenship
Post Office Address		

WO 99/54487

1

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: INSTITUT PASTEUR
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- (C) CITY: PARIS CEDEX 15
- (E) COUNTRY: FRANCE
- (F) POSTAL CODE (ZIP): 75724

(ii) TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA LIBRARY. APPLICATION TO THE DETECTION OF MYCOBACTERIA.

(iii) NUMBER OF SEQUENCES: 5

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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CATTGAGCAT GTCGAGCGTC GCTTCGATGT GAGCGCACCA TTCCGTGTCC AACGATTTC	180
GACGAACATT GAATATTCCA CTCGCGACGC TATAGTCCGC CTCCCGATCT ATGCGCGCCG	240
CGCAGATGAA GTCTGCGTTC GCCCGACCTT CGAAACGTAG TGCGGCCGCG CGCACCATTT	300
CGGGGGAGAC GTCGATGCCG GTGTAATCAG TTTTGAAGCC ACGCGCATCT AGGTAGTCCA	360
GTAGAGCCCC ATAGCCACAG CCTAGATCGT TGATCGAAAA TGGGTCCGCC GCATTGACAA	420
TGCGCACCAG CTGGTCAAAG CGCAACGCCT GCCCGGCTTC GCCGTTCCAA TCGACGCCGC	480
GCGGGTGCCG TGTGCTTCGA GTTTCGATGC GTAGTAACGG GCCACGTCAG CGAGCATGGT	540

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GTCCGAGACT ATACCTTCAA CAGTTGCATG CCGAGGCTGC GGC GGGCAAT GACCCAAAAA 660

CCCCCGGCA CGGTTCCGCG AGCAAGGAAG CGTGGAGACG ATAGATAATT TCACTGGCGA 720

CAGTACCTCA AATAGTCCGG AGCCTCGGCT CCGACGTTAA AGAGCAGATC CAGAATCGAC 780

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TGACGAGTTG GCTCGGATCA TGGTCGACGC GGACATGGCG GCGCTGGAGT GCGAAGGCAA 8040  
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CCGCTTGACC GCGCGGCCCG GGTCTACATC GCCGGGCATC GCGGCCTGGT CCGGTCCGCG 8160  
CTGCTACGCA CGTTTGCGGG CGCGGGGTTC ACCAACCTGC TGGTGCGGTC ACGCGCCGAG 8220  
CTTGATCTGA CGGATCGGGC CGCGACGTTC GACTTCGTTC TCGAGTCGAG GCCGAGGTC 8280  
GTCATCGACG CGGCGGCCCG GGTCGGCGGC ATCCTGGCCA ACGACACCTA CCCGGCCGAT 8340  
TTCCTGTCGG AAAACCTCCA GATCCAGGTC AACCTGCTGG ATGCCGCCGT GGCGGCGCGG 8400  
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ATCCCGGAGA GCGCGCTGCT CACCGGTCCG TTGGAGCCGA CCAACGACGC GTACGCGATC 8520  
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ATCTCGGCGA TGCCACCAA CCTGTACGGG CCAGGCGACA ACTTTTCGCC GTCCGGCTCG 8640  
CATCTGCTGC CGGCACTCAT CCGCCGCTAT GACGAGGCCA AAGCCAGTGG CGCGCCCAAC 8700  
GTGACCAACT GGGGCACCGG CACGCCCCGA CGGGAGTTGC TGACAGTCGA CGACCTGGCG 8760  
AGCGCATGCC TGTATCTGCT GGAACATTTT GACGGGCCGA CCCATGTCAA CGTGGGAACC 8820  
GGCATCGACC ACACCATCGG CGAGATCGCC GAGATGGTCG CCTCGGCGGT AGGCTATAGC 8880  
GGCGAAACCC GCTGGGATCC AAGCAAACCG GACGGAACAC CACGCAAACT GCTGGATGTT 8940  
TCGGTGCTAC GGGAGGCGGG ATGGCGGCCCT TCGATCGCGC TGCGCGACGG CATCGAGGCG 9000  
ACGGTGCGCT GGTATCGCGA GCACGCGGGA ACGGTTCTGGC AATGAGGCTG GCCCGTCGCG 9060





TGGTCGAGAC GATGCTCACC TTGGGGCAAA GCTGGGGACT CACCGTCGGC CCTTTTCCTG 12540  
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 CGTCGTGGCC TGGTGGTCGG CGGACGTACG GCACACGCTG GCGAAGTATA GCGAGGGTGC 12660  
 ACTGACGTTG GGCTCGAACC GCGTGGCGCG CGGTGTGGGC GCACCGTCTC GAGTCGGTGC 12720  
 TGGTTGGCTC GC 12732

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATACTCAAGC TTGCCGCAAT CGAAACCAAC CTGTTTGTGC CGCAAGAAAT TACGCCGTGG 60  
 CCCGGCGCCG ATCAAGAAAC GCCCCGGCGC GCGGCGGTGT CGTCGTATGG CATGACGGGC 120  
 ACCAATGTGC ACGCCATTGT CGAGCAGGCA CCGGTGCCAG CCCCCGAATC CGGTGCACCA 180  
 GGCGACACCC CGGCCACACC CGGTATCGAC GGCGCGCTGC TGTTCGCGCT GTCGGCCAGC 240  
 TCGCAGGACG CGCTGCGGCA AACCGCCGCG CGGCTGGCCG ATTGGGTCT 289

## (2) INFORMATION FOR SEQ ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TTGGCGGGTT GGCCACACAC CCGCCGGTGA CGGCGACGAT GCTGGGCTGG TTGCGGCCCT 60  
 GCGCCACCGC GGCTTGATG CTGGTTGGCT GTCTTGGGAC GATCCCGAAA TAGTCCACGC 120  
 GGATCTGGTG ATTTTGC GGG CTACCCGCGA TTACCCGCG CGGCTCGACG AGTTTTTGGC 180

CTGGACTACC CGCGTGGCCA ATCTGCTGAA CTCGCGGCCG GTGGTGGCCT GGAATGTCCA 240  
CGCCGTTTAC CTACGTGACC TTGATGGGAT CCGGGGGT 278

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CCGACCCAGA CACTGACCGG GCGACCGCTG ATCGGCAACG GCACCCCCGG GGCGGTCGGC 60  
AGCGGGGCCA CCGGGGCCCC CGGTGGGTGG CTGCTCGGCG ACGGCGGGGC CGGCGGGTCC 120  
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GGTGCCGGCG GAGGTCACGG CGGGACCGGC GGGCTCAGCA CTAATGGCGA CGGCGGGGTT 420  
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GGGGCCGGTG GCAACGCCGG GCTGCTGTTG TCCAGCGGCG GGGCCGGCGG GTTCGGCGGG 660  
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GGCACC GGCG GTCAGTTATG GGGTAGCGGC GCGCGCGGCG TCGAAGGCGG CGCAGCCTTA 840  
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